

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 An Unit: _____ Phone Number 30 _____ Serial Number: _____
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If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

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Searcher: Jan

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Final Time: + 10

Type of Search

NA Sequence (#) _____

AA Sequence (#) ☒

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel/Orbit _____

Dr. Link _____

Lexis Nexis _____

Sequence Systems ☒

WWW Internet _____

Other (specify): _____

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:52:29 ; Search time 13.4523 Seconds

(without alignments)
1657.949 Million cell updates/sec

Title: US-09-847-208B-3

Perfect score: 1260
Sequence: 1 EPKSCDKTHTCPPCPAPELL.....MHEALNNHYQORSLSPGK 232

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 1225 | 97.2 | 330 | 1 | Ig gamma-1 chain C |
| 2 | 1219 | 96.7 | 374 | 2 | Ig heavy chain V r |
| 3 | 1217 | 96.6 | 255 | 4 | Ig gamma-1 chain C |
| 4 | 1172 | 93.0 | 234 | 2 | Ig gamma chain C r |
| 5 | 1138 | 90.3 | 377 | 2 | Ig gamma-3 chain C |
| 6 | 1136 | 90.2 | 377 | 2 | Ig gamma-3 chain C |
| 7 | 1123 | 89.1 | 289 | 1 | Ig gamma-3 heavy C |
| 8 | 1107 | 87.9 | 326 | 1 | Ig gamma-2 chain C |
| 9 | 1097 | 87.1 | 327 | 1 | Ig gamma-4 chain C |
| 10 | 883 | 70.1 | 323 | 1 | Ig gamma chain C r |
| 11 | 868.5 | 68.9 | 328 | 2 | Ig gamma 2b chain |
| 12 | 868.5 | 68.9 | 328 | 2 | Ig gamma 2b chain |
| 13 | 868.5 | 68.9 | 328 | 2 | Ig gamma 2b chain |
| 14 | 858 | 68.7 | 277 | 1 | Ig gamma 4 chain C |
| 15 | 847.5 | 67.3 | 328 | 2 | Ig gamma-2 chain C |
| 16 | 840.5 | 66.7 | 328 | 2 | Ig gamma 1 chain C |
| 17 | 820 | 65.1 | 470 | 2 | Ig gamma 3 chain c |
| 18 | 813 | 64.5 | 333 | 2 | Ig heavy chain pre |
| 19 | 812.5 | 64.5 | 329 | 1 | Ig gamma-2b chain C |
| 20 | 811.5 | 64.4 | 308 | 2 | Ig gamma-3 chain C |
| 21 | 811.5 | 64.4 | 472 | 2 | Ig heavy chain C r |
| 22 | 801.5 | 63.6 | 398 | 1 | Ig gamma-1 chain c |
| 23 | 794.5 | 63.1 | 444 | 2 | Ig gamma-3 chain C |
| 24 | 789.5 | 62.7 | 324 | 1 | Ig gamma-1 chain C |
| 25 | 784.5 | 62.3 | 326 | 2 | Ig gamma-1 chain C |
| 26 | 784.5 | 62.3 | 393 | 1 | Ig gamma-1 chain C |
| 27 | 776.5 | 61.6 | 329 | 1 | Ig gamma-2c chain |
| 28 | 776 | 61.6 | 330 | 1 | Ig gamma-2c chain |
| 29 | 776 | 61.6 | 469 | 2 | Ig gamma-2a chain |

| | | | | | | |
|----|-------|------|-----|---|--------|--------------------|
| 30 | 772 | 61.3 | 335 | 1 | G2MSAB | Ig gamma-2a chain |
| 31 | 771 | 61.2 | 399 | 1 | G2MSAW | Ig gamma-2a chain |
| 32 | 761 | 60.4 | 446 | 2 | S40295 | Ig gamma-2a chain |
| 33 | 751.5 | 59.6 | 474 | 1 | G2MS11 | Ig gamma-2b chain |
| 34 | 747.5 | 59.3 | 322 | 2 | PS0019 | Ig gamma-2a chain |
| 35 | 746.5 | 59.2 | 405 | 1 | G2MSBM | Ig gamma-2b chain |
| 36 | 735 | 58.3 | 327 | 2 | S06611 | Ig gamma-2b chain |
| 37 | 731.5 | 58.1 | 475 | 2 | S01321 | Ig gamma-2b chain |
| 38 | 669 | 53.1 | 180 | 2 | I46732 | Ig gamma heavy Cha |
| 39 | 549 | 43.6 | 249 | 2 | S69340 | Ig heavy chain VHI |
| 40 | 547 | 43.4 | 218 | 2 | A36040 | Ig heavy chain V-I |
| 41 | 542 | 43.0 | 152 | 2 | S14236 | Ig gamma-1 chain C |
| 42 | 366.5 | 29.1 | 572 | 2 | B46529 | Ig r heavy chain (|
| 43 | 357 | 28.3 | 549 | 2 | S04845 | Ig heavy chain pre |
| 44 | 353 | 28.0 | 343 | 2 | S25644 | Ig mu chain C regi |
| 45 | 353 | 28.0 | 455 | 1 | MHMS | Ig mu chain C regi |

ALIGNMENTS

RESULT 1

GHHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999

C:Accession: A93433; S36861; S33887; B90563; A90564; B91688; A91233; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <EHL>

A:Cross-references: EMBL:Z17370

A>Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker

A>Note: Lys330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gamma2c-immunoglobulin. VII. Amino acid seq

A:Reference number: A90563; MUID:71064024; PMID:5483771

A:Accession: B90563

A:Contents: myeloma protein Eu

A:Molecule type: protein

A:Residues: 1-96, 'R', 98-135 <CUN>

A>Note: this sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gamma2c-immunoglobulin. VIII. Amino acid se

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2

A>Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R:Ponsingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni

1gen Primaerstruktur
A:Reference number: A91668; MUID:77070269; PMID:8264475
A:Contents: myeloma protein N1e
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', '36-96', 'K', '98-115', 'Q', '117-197', 'D', '199-238', 'D', '240', 'L', '242-268', 'E', '27
A>Note: this sequence has the G1m(17) and G1m(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KOL, disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', '98-197', 'D', '199-238', 'E', '240', 'W', '242-266', 'D', '268-271', 'D', '273-330' <SCH
A>Note: this sequence has the G1m(3) and G1m(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Dieler, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbomide cleavage products, and the disulfide bridges
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Locations: 99/1, 114/1, 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83, 114-204, 250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109, 112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 97.28; Score 1225; DB 1; Length 330;
Best Local Similarity 97.08; Pred. No. 3.9e-86;
Matches 223; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDTHHCPCPAPABELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDSHEDPEVKF 60
|||||
99 EPKSCDTHHCPCPAPABELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDSHEDPEVKF 158
|||||
61 NMVYDGEVHNHVKTKPREEOYNSTRVSVLTVLHQMNGKEKCKVSNKALPAPIEKT 120
|||||
159 NMVYDGEVHNHVKTKPREEOYNSTRVSVLTVLHQMNGKEKCKVSNKALPAPIEKT 218
|||||
121 ISRAKVGPREOYVTLPPSDDELTKNOVSLTCLVKGFPSPDIAVEMWSNQPENNYKTP 180
|||||
219 ISRAKVGPREOYVTLPPSDDELTKNOVSLTCLVKGFPSPDIAVEMWSNQPENNYKTP 278
|||||
181 PVLDSVGSFFLYSKLTVDKSRMOGQNFSCSVHMEALHNHYOQKSLSPGK 232
|||||
279 PVLDSVGSFFLYSKLTVDKSRMOGQNFSCSVHMEALHNHYOQKSLSPGK 330
|||||

RESULT 2
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamilich, A.A.; Aucouturier, P.; Freud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995

A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687; PMID:7744049
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamilich, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', '142-374' <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 96.78; Score 1219; DB 2; Length 374;
Best Local Similarity 96.18; Pred. No. 1.3e-85;
Matches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDTHHCPCPAPABELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDSHEDPEVKF 60
|||||
143 EPKSCDTHHCPCPAPABELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDSHEDPEVKF 202
|||||
61 NMVYDGEVHNHVKTKPREEOYNSTRVSVLTVLHQMNGKEKCKVSNKALPAPIEKT 120
|||||
203 NMVYDGEVHNHVKTKPREEOYNSTRVSVLTVLHQMNGKEKCKVSNKALPAPIEKT 262
|||||
121 ISRAKVGPREOYVTLPPSDDELTKNOVSLTCLVKGFPSPDIAVEMWSNQPENNYKTP 180
|||||
263 ISRAKVGPREOYVTLPPSDDELTKNOVSLTCLVKGFPSPDIAVEMWSNQPENNYKTP 322
|||||
181 PVLDSVGSFFLYSKLTVDKSRMOGQNFSCSVHMEALHNHYOQKSLSPGK 232
|||||
323 PVLDSVGSFFLYSKLTVDKSRMOGQNFSCSVHMEALHNHYOQKSLSPGK 374
|||||

RESULT 3
S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A>Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
R:Fillipa, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene produc
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FTL>
A:Cross-references: EMBL:X70421; NID:933068; PIDN:CAA9866.1; PID:933069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 96.68; Score 1217; DB 4; Length 255;
Best Local Similarity 96.68; Pred. No. 1.1e-85;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

1 EPKSCDTHHCPCPAPABELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDSHEDPEVKF 60
|||||
24 ESKSCDTHHCPCPAPABELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDSHEDPEVKF 83
|||||
61 NMVYDGEVHNHVKTKPREEOYNSTRVSVLTVLHQMNGKEKCKVSNKALPAPIEKT 120
|||||
84 NMVYDGEVHNHVKTKPREEOYNSTRVSVLTVLHQMNGKEKCKVSNKALPAPIEKT 143
|||||
121 ISRAKVGPREOYVTLPPSDDELTKNOVSLTCLVKGFPSPDIAVEMWSNQPENNYKTP 180
|||||
144 ISRAKVGPREOYVTLPPSDDELTKNOVSLTCLVKGFPSPDIAVEMWSNQPENNYKTP 203
|||||

A:Reference number: A92219; MUID:77118561; PMID:402363
A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein A
A:Accession: A92219
A:Molecule type: protein
A:Residues: 12-97 <MIC>
A>Note: the hinge region in gamma-3 chains is about four times as long as in other gamma-3 chains (12-28)
A>Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form intrachain disulfide bonds
R:Wolfenstein-Todell, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71: 907-914, 1976
A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the heavy chain of gamma-3 chains
A:Reference number: A90198; MUID:77021516; PMID:823945
A:Contents: heavy chain disease protein ZUC, partial sequence corresponding to residues 12-97 of protein A
A:Accession: A90198
A:Molecule type: protein
A:Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A>Note: this protein lacks most of the V region, all of the CH1 region, and part of the CH2 region
R:Alexander, A.; Steinmetz, M.; Barltan, D.; Frangione, B.; Franklin, E.C.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A:Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion
A:Reference number: A93915; MUID:82247835; PMID:6808505
A:Contents: heavy chain disease protein Omm
A:Accession: A93915
A:Molecule type: mRNA
A:Residues: 12-70, 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157
A>Note: a carboxyl-terminal Lys is removed posttranslationally
A>Note: this sequence may represent an allelic form or another gamma chain subclass
C:Comment: The heavy chain disease protein wis is shown.
C:Keywords: heavy chain disease
C:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglytamic acid
F:203-270/Domain: immunoglobulin homology <IMM>
F:6/140/Binding site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6/140/Binding site: carbonyl (Asn) (covalent) #status experimental

A>Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J.Immunol. 125, 1048-1054, 1980
A>Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, an
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein T11
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19,'Q','21-57,'Z',59,'A',61-193,'D',195-325 <NAN>
A>Note: Trp 156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can.J.Biochem. 57, 758-767, 1979
A>Title: The amino acid sequences of the three heavy chain constant region domains of
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',1
A>Note: This sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol.Immunol. 16, 923-925, 1979
A>Title: A note on the amino acid sequence of residues 381-391 of human Immunoglobuli
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A>Note: The revised sequence differs from that shown in having 60-Ala and in the amid
ned
R:Milstein, C.; Frangione, B.
Biochem.J. 121, 217-225, 1971
A>Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4960472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A>Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain) disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domains: immunoglobulin homology <IMI>
F:133-202/Domains: immunoglobulin homology <IM2>
F:239-306/Domains: immunoglobulin homology <IM3>
F:14/Disulfide bonds: Interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:109,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

| | Query Match | Best Local Similarity | Matches | Conservative | Mismatches | Indels | Gaps |
|----|-------------|--|---------|--------------|--------------------|--------|-------------|
| Oy | 1 | EPKSCDDTHNCPCPEAPELLGGPSEVFLFPKKPKDTLMISRTPEYTCVVVDVSHEDEVKR | 60 | 87.9% | Score 1107; | DB 1; | Length 326; |
| Db | 99 | ERKCCVE---CPCCAPP-VAGPSVFLEPPRPCKTLMISTREPTCVVVDVSHEDEVOR | 154 | 88.4% | Pred. No. 3.8e-77; | | |
| Oy | 61 | NMYVDGEVHNWAKRKPREEDYNSTYRVVSVLTVLHQMMNGKEKCKVSKNALPAPIEKT | 120 | 12; | | | |
| Db | 155 | NMYVDGEVHNNAKRRPREEDGFNSFRVYSVLTIVHDQMLNGKEKCKVSKNGLPAPIEKT | 214 | | | | |
| Oy | 121 | ISKAVDPREPQVYTLPSPDELTKNOVSLTCLVKGYPDSIDIAVENSGCPENNYKTP | 180 | | | | |

Db 215 ISKTGKQPREQVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVEMESNGPENNYKTPP 274
 QY 181 PVLDSVGSFELSKLTVDKSRMOQGNFSCVMHEALHNHYQOORSLSPGK 232
 Db 275 PMLDSGSFELSKLTVDKSRMOQGNFSCVMHEALHNHYQOORSLSPGK 326

RESULT 9

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 02-Apr-1982 #sequence-revision 02-Apr-1982 #text-change 16-Jul-1999

C:Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 <EHL>

A:Note: the sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant

A:Reference number: A90249; MUID:70207560; PMID:4192699

A:Accession: A90249

A:Molecule type: Protein

C:Genetics: 1-30; 81-326 <PIN>

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1; 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C:Superfamily: Immunoglobulin C region; Immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: Interchain (to light chain) #status experimental

F:27-83;141-201;247-305/Disulfide bonds: #status predicted

F:106;109/Disulfide bonds: Interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 87.1%; Score 1097; DB 1; Length 327;

Best Local Similarity 90.5%; Pred. No. 2.2e-76;

Matches 201; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 11 CPCCPAPPELLGSPVFLPPKPKDTLMSRPEVTCVAVVDSHEDEPKFMYVDGVEVH 70
 Db 106 CPSCPAPPELLGSPVFLPPKPKDTLMSRPEVTCVAVVDSHEDEPKFMYVDGVEVH 165
 QY 71 NVKTRPREQYNSYRVSVLTVLHONMNGKEYCKVSNKALPAPIETKISKAKVQPRE 130
 Db 166 NAKTRPREQFNSTYRVSVLTVLHODMLNGKEYCKVSNKGLPSSIKETISKAKGQPRE 225
 QY 131 POYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGPENNYKTPPVLDSVGSF 190
 Db 226 POYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGPENNYKTPPVLDSVGSF 285
 QY 191 LYSKLTVDKSRMOQGNFSCVMHEALHNHYQOORSLSPGK 232
 Db 286 LYSKLTVDKSRMOQGNFSCVMHEALHNHYQOORSLSPGK 327

RESULT 10

GHRB

Ig gamma chain C region - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 24-Apr-1984 #sequence-revision 15-Nov-1984 #text-change 16-Jul-1999

C:Accession: A91749; A90290; A93928; A90245; A94416; A02161

R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
 Immunogenetics 18, 387-397, 1983
 A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-1 hap
 A:Reference number: A91749; MUID:84030930; PMID:6313520

A:Accession: A91749

A:Molecule type: mRNA

A:Residues: 1-323 <BER>

A:Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-

R:Pratt, D.M.; Mole, L.E.

Biochem. J. 151, 337-349, 1975

A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunog

A:Reference number: A90290; MUID:76135469; PMID:1243651

A:Accession: A90290

A:Molecule type: Protein

A:Residues: 1-47; 'E', 49-71, 'PV', 72-128 <PRA>

R:Martens, C.L.; Moore, K.W.; Stelmets, M.; Hood, L.; Knight, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982

A:Title: Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma heavy ch

A:Reference number: A93928; MUID:83299917; PMID:6193512

A:Accession: A93928

A:Molecule type: mRNA

A:Residues: 88-103; 'W', 105-143; 'E', 145-184; 'A', 186; 'E', 188-266 <MAR>

A:Cross-references: GB:M6426; NID:9165111; PIDN:AA31289.1; PID:9165112

A:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic ma

R:Frutcher, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.

Biochem. J. 116, 249-259, 1970

A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobul

A:Reference number: A90245; MUID:70110015; PMID:5461106

A:Accession: A90245

A:Molecule type: Protein

A:Residues: 132-143; 'E', 145-161 <FRU>

R:Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.

In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wikse

A:Reference number: A94416

A:Accession: A94416

A:Molecule type: Protein

A:Residues: 129-131;155-172; 'D', 174-184; 'A', 186; 'E', 188-200; 'D', 202-217; 'E', 219-232; 'A:Note: this has the e15 allotypic marker, 185-Ala

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: Immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-82/Domain: immunoglobulin homology <IM1>

F:130-199/Domain: immunoglobulin homology <IM2>

F:236-303/Domain: immunoglobulin homology <IM3>

F:173/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 70.1%; Score 883; DB 1; Length 323;

Best Local Similarity 64.5%; Pred. No. 4.5e-60;

Matches 160; Conservative 34; Mismatches 38; Indels 16; Gaps 2;

QY 1 EPKSGDKH-----TC--PPCAPPELLGSPVFLPPKPKDTLMSRPEV 44
 Db 76 QPVTGVNAHPATNTKVDKTVAPSTCSKPTCPPELLGSPVFLPPKPKDTLMSRPEV 135
 QY 45 TCVVVDVSHDEPEVKFMYVDGVEVHNKTRPREQYNSYRVSVLTVLHONMNGKEY 104
 Db 136 TCVVVDVSDDEPEVFTMYINNGEYRTARPLRQGFNSTLRVSTLTLDQDMRGKEF 195
 QY 105 KCKVSNKALPAPIETKISKAKVQPREQYNSYRVSVLTCLVKGFYPSDIAV 164
 Db 196 KCKVSNKALPAPIETKISKAKVQPREQYNSYRVSVLTCLVKGFYPSDIAV 255
 QY 165 EMESNGPENNYKTPPVLDSVGSFELSKLTVDKSRMOQGNFSCVMHEALHNHYQOR 224
 Db 256 EMESNGPENNYKTPPVLDSVGSFELSKLTVDKSRMOQGNFSCVMHEALHNHYQOR 315
 QY 225 SLSPGK 232
 Db 316 SLSPGK 323

RESULT 11

147160
 Ig gamma 2b chain constant region - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: I47160
 R:Kasckovics, L.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3563-3573, 1994.
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
 A:Reference number: 147158; MUID:95015845; PMID:7930579
 A:Accession: I47160
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Stem: 1-328 <KAC>
 A:Molecule type: mRNA
 A:Residues: 1-328 <KAC>
 A:Cross-references: EMBL:U03780; NID:g433125; PIDN:AA652218.1; PID:g433126
 C:Genetics:
 A:Gene: I9G2b
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 P:133-202/Domain: immunoglobulin homology <IMM>

| | | | | |
|-----------------------|------------------|--------------------|-----------|-------------|
| Query Match | 68.9%; | Score 868.5; | DB 2; | Length 328; |
| Best Local Similarity | -70.1%; | Pred. NO. 5.9e-59; | | |
| Matches 157; | Conservative 32; | Mismatches 32; | Indels 3; | Gaps 2; |

```
D6      225   P...VYLTLP...P...HAEELSSRSKVSITCLTGLVGFPPDIDIVEMQRNGOPEPEGNYRTTPPQQDVDSG 284
Q7      169   FFLYSKLTVDRSKRMWGOGNWFSCVMHEALHNHYAORSLSLSGCK 232
Db      285   YFLYKFSVDKASWMOGGIFOCAMVHEALHNHTYTSISKTPEK 328

RESULT 13
I47162
Ig gamma 4 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47162
R:Kacs Kovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
Article: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number:I47158; MUID:95015845; PMID:7930579
```

A1:Cross-references: EMBL:U03782; NID:g433129; PIDD:AAA52220.1; PID:g433130
 C:Genetics:
 A1:Gene: IgG4
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:82-151/Domain: immunoglobulin homology <IMM>

| | | | | |
|-----------------------|-----------------|-------------------|----------|------------|
| Query Match | 68.7% | Score 865 | DB 2 | Length 277 |
| Best Local Similarity | 69.0% | Pred. No. 8.9e-59 | | |
| Matches 158 | Conservative 32 | Mismatches 35 | Indels 4 | Gaps 3 |

| | | | |
|----|-----|--|-----|
| OY | 131 | PÖVTLPPRSBELKRNQVSLTCLVAKGFPSPISIAVEEMNCG - DENNKKTTPVLVDVGSGS | 188 |
| | | : : : : : : : : : : : : : : : | |
| Dd | 225 | PÖVTLRPHAEILSRSKSVICLIVIGFRPPIIDVEMQNCGPREDBGNRTTRIPPOODVDGT | 284 |
| Oy | 189 | FELYSKLTVDRSMQOGNVESCSVMHEALNNHYOORSLISLSPKG | 232 |
| | | : : : : : : : : : : : : : : : | |
| Dd | 285 | YFLSKFSEYDASWAGGIIFQCAVMHEALNNHYÖKSTLSIKRPBG | 328 |

```

0y      8  THCPDPP-APELLG-GPSVFLRPPKDTLMSRPDVTGVVDVSDHDEPKFNMWYD  65
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     49  TKTPRCDIPACGEGPSAFIRPPKRDTLMSRPPKVTGVVDVSDHDEPKFNMWYD  10
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
0y     66  GVEVHNANKTPRBDQVNSTRVVSVLTVLHÖMMNMNGKEKCKVSKALPDLKTIISAK  12
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```
RESULT 12
147159
Iq gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
#Accession: F43150
```

[illegible]

A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C:Genetics:
A:Gene: IgG2a
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
C:i33-202/Domain: Immunoglobulin homology <TM>

RESULT 14
G2GP
Tg gamma-2 chain C region - guinea pig
C:Species: *Cavia porcellus* (guinea pig)
C:Date: 07-May-1991 #sequence-revision 07-May-1991 #text-change 16-Jul-1999.
A:Accession: A94553; A90352; A90359; A90384; A90385; A02151
R:Trischmann, T.M.
Submitted to the Atlas, April 1975
A:Reference number: A94553
A:Accession: A94553

| | | | | |
|---------------------------|-------|-------------------|-----------|------------|
| Query Match | 68.9% | Score 868.5 | DB 2 | Length 328 |
| Best Local Similarity | 70.1% | Pred. No. 5.9e-59 | | |
| Matches 157; Conservative | 32; | Mismatches 32; | Indels 3; | Gaps 2 |

R. Birshtein, B. K.; Hussain, Q. Z.; Cebra, J. J. *Biochemistry* 10, 18-25, 1971

QY 11 CPGCPAPETLGGSVFLFPFKPKPTLMTSRTPEVTCVAVDVSHEDEVEYNNYVDGVEVH 70
106 CPGCPACE-SPGGSVFIFPPPKPKDTLMTSRTPOVTCVAVDVSQDEPEVFSWYVDGVEVH 164

A:Accession: A90352
A:Molecule type: protein

```

QY      71 NVKTRPREQNSTYRVSVLYLHÖMMNGKEYCKVSNKALPAPIEKTISKAVQPRE 130
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
166  MIOGNEPPOVEMVUUCUUCUUCUUCUUCUUCUUCUUCUUCUUCUUCUUCUUCUUCUUCUUC

```

R; Turner, K.J.; Cebra, J.J. *Biochemistry* 10, 9-17, 1971

131 PÖVNTLPPSRBELTKNOVSITLCVKGFEVPSDIAWESNGO -- PENNYKTTTPVLDSYGS 188

A: Reference number: A90359; MUID: 71058486; PMID: 5538616
A: Accession: A90359

A:Molecule type: protein
A:Residues: 69-133;312-329 <TUR>
R:Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90384; MUID:75036072; PMID:4429665
A:Accession: A90384
A:Molecule type: protein
A:Residues: 134-226 <TRA>
R:Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90385; MUID:75036073; PMID:4609467
A:Accession: A90385
A:Molecule type: protein
A:Residues: 227-311 <TR2>
R:Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A:Reference number: A90354; MUID:71058474; PMID:4922544
A:Contents: annotation: disulfide bonds
A:Note: Cys-16 is involved in a heavy-light chain bond
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds.
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:21-81/Domain: immunoglobulin homology <IM1>
F:135-204/Domain: immunoglobulin homology <IM2>
F:241-310/Domain: immunoglobulin homology <IM3>
F:28-79/Disulfide bonds: #status experimental
F:142-202/Disulfide bonds: #status experimental
F:178/Binding site: carbohydrate (asn) (covalent) #status experimental
F:248-308/Disulfide bonds: #status experimental

Query Match 68.1%; Score 858; DB 1; Length 329;
Best Local Similarity 67.4%; Pred. No. 3.8e-58;
Matches 157; Conservative 28; Mismatches 42; Indels 6; Gaps 2;

OY 1 EPKSDKTHTCPPAPAPLLGSPSYFLPPPKKDTLMISRTPEVTCVVDVSHEDPEYKF 60
Db 101 ZPBPC---TCPCPCPPENLGGPSVFIPPKPKDTLMISLTPRYTCVVDVSDDEPVOF 156
OY 61 NMVYDGVENVHVKTPREQYNSTRYVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKT 120
Db 157 TWFDNKRPNVGNATKPRVEQYINTTRVESVLPIDHDMRGKEKCKVNNKALPAPIEKT 216
OY 121 ISKAKVQPREQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--ENNYKT 178
Db 217 ISKTKGAPRMFDVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--ENNYKT 276
OY 179 TTPVLDVSGSFLLYSKLTVDKSRMOQGVNFCVNMHEALHNHYOQRLSLSPG 231
Db 277 TTPLEDADGSYFLYSKLTVDKSRMOQGVNFCVNMHEALHNHYOQRLSLSPG 329

RESULT 15

147158
Ig gamma 1 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: 147158
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: 147158; MUID:95015845; PMID:7930579
A:Accession: 147158
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-References: EMBL:U03778; NID:9433121; PIDN:AAA52216.1; PID:9433122
C:Genetics:

A:Gene: IgG1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IM1>

Query Match 67.3%; Score 847.5; DB 2; Length 328;
Best Local Similarity 69.3%; Pred. No. 2.4e-57;
Matches 156; Conservative 30; Mismatches 36; Indels 3; Gaps 2;

OY 10 TCPCPAPAPLLGSPSYFLPPPKKDTLMISRTPEVTCVVDVSHEDPEYKFNWVDGVEV 69
Db 105 TCPICPGCE-VAGSSVFIFPPPKKDTLMISOTPEVTCVVDVSHEDPEYKFNWVDGVEV 163
OY 70 HNVKTPREQYNSTRYVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKTISRAKYQPR 129
Db 164 HTAETRPKEQFNSTRYVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKTISRAKYQPR 223
OY 130 EPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--PENNYKTPPYLDSVG 187
Db 224 EPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--PENNYKTPPYLDSVG 283
OY 188 SFELYSKLTVDKSRMOQGVNFCVNMHEALHNHYOQRLSLSPG 232
Db 284 TFFLYSKLAVDKARMDHGDKECAVMHEALHNHYOQRLSLSPG 328

Search completed: July 15, 2003, 06:59:31
Job time: 14.4523 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:47:19 ; Search time 7.24353 Seconds
(without alignments)
1328.428 Million cell updates/sec

Title: US-09-847-208b-3

Perfect score: 1260

Sequence: 1 EPKSCDKTRHCPAPPELL.....MHEALHNHYQORSLSLSPGK 232

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1225 | 97.2 | 330 | 1 | GCL_HUMAN |
| 2 | 1128 | 89.5 | 290 | 1 | GC3_HUMAN |
| 3 | 1107 | 87.9 | 326 | 1 | GC2_HUMAN |
| 4 | 1097 | 87.1 | 327 | 1 | GC4_HUMAN |
| 5 | 883 | 70.1 | 323 | 1 | GC_RABIT |
| 6 | 858 | 68.1 | 329 | 1 | GC2_CAVPO |
| 7 | 813 | 64.5 | 333 | 1 | GCB_RAT |
| 8 | 812.5 | 64.5 | 329 | 1 | GC3_MOUSE |
| 9 | 801.5 | 63.6 | 398 | 1 | GC3M_MOUSE |
| 10 | 789.5 | 62.7 | 324 | 1 | GCL_MOUSE |
| 11 | 784.5 | 62.3 | 326 | 1 | GCL_RAT |
| 12 | 784.5 | 62.3 | 393 | 1 | GCLM_MOUSE |
| 13 | 776.5 | 61.6 | 329 | 1 | GCB_RAT |
| 14 | 776 | 61.6 | 330 | 1 | GCA_MOUSE |
| 15 | 772 | 61.3 | 335 | 1 | GCB_MOUSE |
| 16 | 771 | 61.2 | 399 | 1 | GCB_MOUSE |
| 17 | 751.5 | 59.6 | 336 | 1 | GCB_MOUSE |
| 18 | 747.5 | 59.3 | 322 | 1 | GCA_RAT |
| 19 | 746.5 | 59.2 | 405 | 1 | GCB_MOUSE |
| 20 | 353 | 28.0 | 455 | 1 | MOC_MOUSE |
| 21 | 347 | 27.5 | 454 | 1 | MOC_HUMAN |
| 22 | 345 | 27.4 | 476 | 1 | MOC_HUMAN |
| 23 | 343 | 27.2 | 476 | 1 | MOC_MOUSE |
| 24 | 339 | 26.9 | 458 | 1 | MOC_RABIT |
| 25 | 334 | 26.5 | 429 | 1 | EPIC_RAT |
| 26 | 333 | 26.4 | 428 | 1 | EPIC_HUMAN |
| 27 | 332 | 26.3 | 421 | 1 | EPIC_MOUSE |
| 28 | 329 | 26.1 | 479 | 1 | MOCM_RABIT |
| 29 | 325 | 25.8 | 450 | 1 | MOC_CANFA |
| 30 | 323 | 25.6 | 454 | 1 | MOC_MESAU |
| 31 | 318 | 25.2 | 457 | 1 | MOC_SUNMU |
| 32 | 297 | 23.6 | 438 | 1 | HVC2_HETER |
| 33 | 293.5 | 23.3 | 299 | 1 | ALC_RABIT |

| | | | | | | |
|----|-------|------|-----|---|------------|--------------------|
| 34 | 287.5 | 22.8 | 438 | 1 | HVC2_HETER | P23087 heterodontu |
| 35 | 277.5 | 22.0 | 461 | 1 | HVC2_HETER | P23088 heterodontu |
| 36 | 276.5 | 21.9 | 393 | 1 | HVC2_HETER | P23089 heterodontu |
| 37 | 275.5 | 21.9 | 446 | 1 | MOC_CHICK | P23084 gallus gall |
| 38 | 267 | 21.2 | 370 | 1 | HVC1_HETER | P23084 heterodontu |
| 39 | 251.5 | 20.0 | 353 | 1 | ALC1_GORGO | P20758 gorilla gor |
| 40 | 251 | 19.9 | 353 | 1 | ALC1_HUMAN | P01876 homo sapien |
| 41 | 247 | 19.6 | 340 | 1 | ALC2_HUMAN | P01876 homo sapien |
| 42 | 243.5 | 19.3 | 344 | 1 | ALC_MOUSE | P01878 mus musculu |
| 43 | 236.5 | 18.8 | 481 | 1 | MOCM_ICPUP | P23735 ictalurus p |
| 44 | 168.5 | 13.4 | 105 | 1 | LAC1_MOUSE | P01843 mus musculu |
| 45 | 167 | 13.3 | 104 | 1 | LAC2_RAT | P20767 rattus norv |

ALIGNMENTS

| RESULT 1 | ID | GC1_HUMAN | STANDARD: | PRT: | 330 AA. |
|----------|--|-----------|-----------|------|---------|
| AC | P01857: | | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | | |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update) | | | | |
| DE | Ig gamma-1 chain C region. | | | | |
| GN | IGHG1. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=82274238; PubMed=6287432; | | | | |
| RA | Ellison J.W., Berson B.J., Hood L.E.; | | | | |
| RT | "The nucleotide sequence of a human immunoglobulin C gamma1 gene."; | | | | |
| RL | Nucleic Acids Res. 10:4071-4079(1982). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE OF 1-135 (MYELOMA PROTEIN EU). | | | | |
| RX | MEDLINE=71064024; PubMed=5489771; | | | | |
| RA | Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.; | | | | |
| RT | Waxdal M.J., Edelman G.M.; | | | | |
| RL | "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; | | | | |
| RN | Biochemistry 9:3161-3170(1970). | | | | |
| RP | [3] | | | | |
| RP | SEQUENCE OF 136-329 (EU). | | | | |
| RX | MEDLINE=71064025; PubMed=5530842; | | | | |
| RA | Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.; | | | | |
| RT | Edelman G.M.; | | | | |
| RL | "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; | | | | |
| RN | Biochemistry 9:3171-3181(1970). | | | | |
| RP | [4] | | | | |
| RP | SEQUENCE (MYELOMA PROTEIN NIE). | | | | |
| RX | MEDLINE=7070269; PubMed=826475; | | | | |
| RA | Ponstingl H., Hilschmann N.; | | | | |
| RT | "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."; | | | | |
| RL | Hope-Seyler's Z. Physiol. Chem. 357:1571-1604(1976). | | | | |
| RN | [5] | | | | |
| RP | SEQUENCE (MYELOMA PROTEIN KOL). AND DISULFIDE BONDS. | | | | |
| RX | MEDLINE=83289131; PubMed=6884994; | | | | |
| RA | Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; | | | | |
| RT | "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."; | | | | |
| RL | Hope-Seyler's Z. Physiol. Chem. 364:713-747(1983). | | | | |
| RN | [6] | | | | |
| RP | DISULFIDE BONDS. | | | | |
| RX | MEDLINE=71064027; PubMed=4923144; | | | | |
| RA | Gall W.E., Edelman G.M.; | | | | |
| RT | "The covalent structure of a human gamma G-immunoglobulin. X. | | | | |

RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196(1970).
 RN (7)
 RP DISULFIDE BONDS.
 RA MEDLINE=77070267; PubMed=1002129;
 RT Dreker L., Schwarz J., Reiche W., Hilschmann N.;
 "Role of antibody structure. The primary structure of a monoclonal
 RT 19g1 immunoglobulin (myeloma protein Nle), I: purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN (8)
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RA MEDLINE=8108100; PubMed=7236608;
 RT Deisenhofer J.;
 "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & ED SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155,166,177,195,198,269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: J00228; AAC82527.1; ALT_INIT.
 DR PIR: A02146; GHUO.
 DR PDB: 1FC1; 15-JUL-92.
 DR PDB: 1FC2; 15-JUL-92.
 DR Genew: HGNC:5525; IGHG1.
 DR MIM: 147100; -
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_G1.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig_3.
 DR SMART: SM00410; Ig_Like; 1.
 DR SMART: SM00407; IgG1; 2.
 DR PROSITE: PS00290; IG_MHC; 2.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 98 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 308
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT STRAND 123 126

FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 148
 FT STRAND 158 162
 FT TURN 163 164
 FT STRAND 165 166
 FT STRAND 175 178
 FT STRAND 183 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 206
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 240
 FT TURN 241 242
 FT STRAND 245 256
 FT STRAND 260 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 324
 SQ SEQUENCE 330 AA; 36106 MW; 3770E106C2FA33D CRC64;
 Query Match 97.2%; Score 1225; DB 1; Length 330;
 Best Local Similarity 97.0%; Pred. No. 1e-93;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDDTHPCPCPAPAPLGGPSVFLFPKPKDTLMSRPEVTCVVDVSHDPEK 60
 DB 99 EPKSCDDTHPCPCPAPAPLGGPSVFLFPKPKDTLMSRPEVTCVVDVSHDPEK 158
 QY 61 NMVYDGVENVHAKKPREEOYNSTYRVSVLTVDHOMMNGEKCKVSNALPAPIEKT 120
 DB 159 NMVYDGVENVHAKKPREEOYNSTYRVSVLTVDHOMMNGEKCKVSNALPAPIEKT 218
 QY 121 ISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTP 180
 DB 219 ISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTP 278
 QY 181 PVLDSGSEFLYSKLTVDKSRWOGGNVFGSCVMHEALHNHYOQSLSPGK 232
 DB 279 PVLDSGSEFLYSKLTVDKSRWOGGNVFGSCVMHEALHNHYOQSLSPGK 330
 RESULT 2
 GC3_HUMAN STANDARD; PRT: 290 AA.
 AC P01860; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
 GN IGHG3
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (DISEASE PROTEIN WIS).
 RA MEDLINE=81021548; PubMed=6774747;
 RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
 RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
 RT gamma 3 heavy-chain disease protein WIS.";
 RL Biochemistry 19:4304-4308(1980).

| | | | | | |
|----|---|---|----------------|------------------|--------------------------------------|
| FT | DISULFID | 39 | 39 | | INTERCHAIN (WITH HEAVY CHAIN DIMER). |
| FT | DISULFID | 42 | 42 | | INTERCHAIN (WITH HEAVY CHAIN DIMER). |
| FT | DISULFID | 48 | 48 | | INTERCHAIN (WITH HEAVY CHAIN DIMER). |
| FT | DISULFID | 54 | 54 | | INTERCHAIN (WITH HEAVY CHAIN DIMER). |
| FT | DISULFID | 57 | 57 | | INTERCHAIN (WITH HEAVY CHAIN DIMER). |
| FT | DISULFID | 63 | 63 | | INTERCHAIN (WITH HEAVY CHAIN DIMER). |
| FT | DISULFID | 69 | 69 | | INTERCHAIN (WITH HEAVY CHAIN DIMER). |
| FT | DISULFID | 72 | 72 | | INTERCHAIN (WITH HEAVY CHAIN DIMER). |
| FT | CARBOHYD | 140 | 140 | | N-LINKED (GLCNAC...). |
| FT | MOD_RRS | 290 | 290 | | REMOVED POST-TRANSLATIONALLY. |
| FT | VARIANT | 126 | 127 | | QV -> EB (IN ZUC). |
| FT | VARIANT | 134 | 134 | | /FtId=VAR_003890. |
| FT | VARIANT | 139 | 139 | | P -> L (IN OMM). |
| FT | VARIANT | 182 | 182 | | F -> Y (IN OMM). |
| FT | VARIANT | 227 | 227 | | /FtId=VAR_003892. |
| FT | VARIANT | 227 | 227 | | T -> A (IN OMM). |
| FT | VARIANT | 227 | 227 | | /FtId=VAR_003893. |
| FT | VARIANT | 227 | 227 | | S -> N (IN OMM). |
| FT | VARIANT | 227 | 227 | | /FtId=VAR_003894. |
| FT | VARIANT | 279 | 279 | | MISSING (IN ZUC). |
| FT | VARIANT | 279 | 279 | | /FtId=VAR_003895. |
| FT | VARIANT | 279 | 279 | | F -> Y (IN OMM). |
| FT | VARIANT | 279 | 279 | | /FtId=VAR_003896. |
| SO | SEQUENCE | 290 AA; | 32331 MM; | E69C8C95705B2F46 | CRC64; |
| | Query Match | Best Local Similarity | 89.5%; | Score 1128; | DB 1; Length 290; |
| | Matches | 205; Conservative | 88.4%; | Pred. No | 8.3e-86; |
| | | | 14; Mismatches | 13; Indels | 0; Gaps |
| QY | 1 | EPKSCDKTHNCPCPAPPELLGSPVFLEPPPKDKTLMISRTPEVTGVVDVSHDEPEYKF | 60 | | |
| Dd | 59 | EPKSCDPHPPCPRCPAPELLGGPSVFLFPFKDKTLMISRPEVTGVVDVSHDEPEVOF | 118 | | |
| QY | 61 | NMYVDGYEVHNVKTRPREOVNSURYRVSVLTIVLHONMNGKEVKCKYSNKALPAPIEKT | 120 | | |
| Dd | 119 | KMYVDGYOVHNAKKRPBQQNSTRFRVSVLTIVLHONMLDSKEKYCKYSNKALPAPIEKT | 178 | | |
| QY | 121 | ISKAKVOPREPOVYTLTPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTPP | 180 | | |
| Dd | 179 | ISKTKGQPREPOVYTLTPPSRBEMTKNQVSLTCLVKGFPSPDIAYEWESSGOPENNYNTPP | 238 | | |
| QY | 181 | PVLDSVGSEFLYLSKLTYDKSRWOGGNPFSCSVMHEALHNHQOSLSLSPSK | 232 | | |
| Dd | 239 | PMLDSDSGFLYLSKLTYDKSRWOGGNLFCSVMHEALHNRTOKSLSLSPSK | 290 | | |
| | RESULT 3 | | | | |
| ID | GC2_HUMAN | STANDARD: | PRT: | 326 AA. | |
| DC | P01859; | | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | | |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update) | | | | |
| GN | Ig gamma-2 chain C region. | | | | |
| OS | IGHG2. | | | | |
| OC | Homo sapiens (Human). | | | | |
| CC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| CC | Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. | | | | |
| RX | NCBI_TaxID=9606; | | | | |
| RX | [1] | | | | |
| RP | SEQUENCE OF 2-326 FROM N.A. | | | | |
| RX | MEDLINE=82197621; PubMed=6804948; | | | | |
| RA | Ellison J.W., Hood L.E.; | | | | |
| RT | "Linkage and sequence homology of two human immunoglobulin gamma | | | | |
| RL | heavy chain constant region genes."; | | | | |
| RN | Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982). | | | | |
| RP | [2] | | | | |
| RC | SEQUENCE OF 88-115 FROM N.A. | | | | |
| RX | TISSUE=Fetal Liver; | | | | |
| RX | MEDLINE=83001943; PubMed=6811139; | | | | |
| RA | Yakahashi N., Ueda S., Obata M., Nakai T., Honjo T.; | | | | |
| RT | "Structure of human immunoglobulin gamma genes: Implications for | | | | |

evolution of a gene family." ;
 Cell 29:671-679(1982).
 [3]
 SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 TISSUE-Fetal Liver;
 MEDLINE=84235992; PubMed=6329676;
 Krawinkel U., Rabbitts T.H.;
 "Comparison of the hinge-coding segments in human immunoglobulin gamma
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 genes." ;
 EMBO J. 1:403-407(1982).
 [4]
 SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 MEDLINE=81007873; PubMed=6774012;
 Wang A.-C., Tung E., Fudenberg H.H.;
 "The primary structure of a human IgG2 heavy chain: genetic,
 evolutionary, and functional implications." ;
 J. Immunol. 125:1048-1054(1980).
 [5]
 SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 MEDLINE=80001357; PubMed=113060;
 Conneil G.E., Parr D.M., Hofmann T.;
 "The amino acid sequences of the three heavy chain constant region
 domains of a human IgG2 myeloma protein." ;
 Can. J. Biochem. 57:758-767(1979).
 [6]
 SEQUENCE OF 238-275 (ZIE).
 MEDLINE=80114419; PubMed=118920;
 Hofmann T., Parr D.M.;
 "A note of the amino acid sequence of residues 381-391 of human
 immunoglobulin gamma chains." ;
 Mol. Immunol. 16:923-925(1979).
 [7]
 REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 Hofmann T., Parr D.M.;
 Submitted (MAR-1980) to the PIR data bank.
 [8]
 SEQUENCE OF 1-121 (DOY).
 MEDLINE=95255298; PubMed=7737190;
 Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins." ;
 Eur. J. Biochem. 228:886-893(1995).
 [9]
 DISULFIDE BONDS.
 MEDLINE=72033500; PubMed=4940472;
 Milstein C., Frangione B.;
 "Disulphide bridges of the heavy chain of human immunoglobulin G2." ;
 Biochem. J. 121:217-225(1971).
 [10]
 DISULFIDE BONDS.
 MEDLINE=69064124; PubMed=5782707;
 Frangione B., Milstein C., Pink J.R.L.;
 "Structural studies of immunoglobulin G." ;
 Nature 221:145-148(1969).

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 or send an email to license@isb-sib.ch).

 EMBL: J00230; AAB59393.1; -
 PIR: A02148; G2HU.
 HSSP: P01857; IFC1.
 Genew: HGNC:5526; IGHG2.
 MIM: 147110; -
 InterPro: IPR003006; Ig_MHC.
 InterPro: IPR003597; Ig_cl.
 InterPro: IPR003600; Ig_like.
 Pfam: PF00047; Ig; 3.

DR SMART: SMO0410; IG-like: 1.
DR SMART: SMO0407; IG1: 2.
DR PROSITE; PS00290; IG-MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINEE.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 246 304
FT SITE 156 156
FT SITE 156 156
FT MOD_RES 326 326
FT VARIANT 60
FT CONFLICT 109 109
SQ SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
Query Match Best Local Similarity 87.9%; Score 1107; DB 1; Length 326;
Matches 205; Conservative 12; Mismatches 11; Indels 4; Gaps 2;
1 EPRKCDTHHCPPPPAPPELLGSGVFLPPPKPDKTLMISRPETVCYVVDVSHDDPEYKF 60
Db 99 ERKCCVE---CPPCAPP-VAGPSVFELPPPKDITLMSRTEVTCVVDVSHDDPEYQF 154
QY 61 NMVYDGEVHNHVKTRPREEOYNSTYRVVSVLTVLHONMMNGKEKCKVSNKALPAPIEKT 120
Db 155 NMVYDGEVHNHAKTKPREEOGNSFTFRVSVYLTVHODLNGKEKCKVSNKGLPAPIEKT 214
QY 121 ISKAKVQPREQVYTLTPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPP 180
Db 215 ISKRRGQPREQVYTLTPSRREMTKKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPP 274
QY 181 PVLDSVGSFFLYSKLTYDKSRMOQGNFYSCSVMEHALHNHQQKSLSTLSPK 232
Db 275 PMLDSGSFFLYSKLTYDKSRMOQGNFYSCSVMEHALHNHTQKSLSTLSPK 326
RESULT 4
GC4_HUMAN GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 1g gamma-4 chain C region.
GN IGHC4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; Pubmed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNM 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; Pubmed=4192699;
RA Plick J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RL Blochem. J. 117:33-47(1970).
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 CC -----
 DR EMBL; K01316; AAB59394.1; ALT_INIT.
 DR PIR; A02150; GAHU.
 DR HSSP; P01842; 7FAB.
 DR Genew; HGNC:5528; IGHG4.
 DR MIM; 147130; -
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003600; Ig-like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; Ig-like; 1.
 DR SMART; SM00407; Igcl; 2.
 DR PROSITE; PS00290; Ig_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 220 CH2.
 FT DOMAIN 221 327 CH3.
 FT DISULFD 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFD 27 83 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFD 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFD 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFD 141 201
 FT DISULFD 247 305
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;
 Query Match 87.1%; Score 1097; DB 1; Length 327;
 Best Local Similarity 90.5%; Pred. No. 3.4e-83;
 Matches 201; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
 QY 11 CPCCPAPPELLGSPVFLPPPKDKTLMISRTPEVTCVVDVSHDEPEKFMVYDGVVH 70
 DB 106 CPSCCAPPEFLGSPVFLPPPKDKTLMISRTPEVTCVVDVSHDEPEKFMVYDGVVH 165
 QY 71 NWTKRPDEQYNSTYRVSVLTVLHONMNGEKYKSNKALPAPIEKTISKAKVDPRE 130
 DB 166 NAKTKRPDEQYNSTYRVSVLTVLHONMNGEKYKSNKALPAPIEKTISKAKVDPRE 225
 QY 131 PÖVTLPPSDEIFRKNÖVSLTCLVKGFPSPDIAYWESNGOPENNYKTPPVLDVSGSEF 190
 DB 226 PÖVTLPPSDEIFRKNÖVSLTCLVKGFPSPDIAYWESNGOPENNYKTPPVLDVSGSEF 285
 QY 191 LYSKLTVDKSRMOQGNVFSQSVMEALHNHYQOQSLSLSPGK 232
 DB 286 LYSRLTVDKSRMOQGNVFSQSVMEALHNHYQOQSLSLSPGK 327
 RESULT 5
 GC_RABIT STANDARD; PRT; 323 AA.
 AC P01870;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma chain C region.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI-Taxid=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84030930; PubMed=6313520;
 RA Bernstein K.E., Alexander C.B., Wade R.G.;
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
 F-1 haplotype";
 RL Immunogenetics 18:387-397(1983).

RN [2]
 RP SEQUENCE OF 1-128.
 RX MEDLINE=76135469; PubMed=1243651;
 RA Pratt D.M., Mole L.E.;
 RT "Sequence studies on the constant region of the Fd sections of rabbit
 immunoglobulin G of different allotype.";
 RT Biochem. J. 151:337-349(1975).
 RN [3]
 RP SEQUENCE OF 88-266 FROM N.A.
 RX MEDLINE=83299917; PubMed=6193512;
 RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
 RT "Heavy chain genes of rabbit IgG: Isolation of a cDNA encoding gamma
 heavy chain and identification of two genomic C gamma genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
 RN [4]
 RP SEQUENCE OF 132-161.
 RX MEDLINE=70110015; PubMed=5461106;
 RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
 RT "Sequence studies of the Fd section of the heavy chain of rabbit
 immunoglobulin G.";
 RL Biochem. J. 116:249-259(1970).
 RN [5]
 RP SEQUENCE OF 129-131 AND 155-322.
 RA Hill R.L., Lebowitz H.E., Fellows R.E. Jr., Delaney R.;
 RL (in) Killander J. (eds.);
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
 Stockholm (1967).
 CC -I- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER.
 CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
 CC MARKERS AND REF.5 THE E15 MARKER.
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 CC -----
 DR EMBL; M16426; AAA31289.1; -
 DR PIR; A02161; GHR.
 DR HSSP; P01857; IFC1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig-cl.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00407; Igcl; 2.
 DR PROSITE; PS00290; Ig_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT VARIANT 104 104 T -> M (IN D11 MARKER).
 FT VARIANT 185 185 T -> A (IN E15 MARKER).
 FT CONFLICT 48 48 N -> E (IN REF. 2).
 FT CONFLICT 71 71 V -> VPY (IN REF. 2).
 FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
 FT CONFLICT 173 173 N -> D (IN REF. 5).
 FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
 FT CONFLICT 201 201 N -> D (IN REF. 5).
 FT CONFLICT 218 218 O -> E (IN REF. 5).
 FT CONFLICT 233 233 E -> Q (IN REF. 5).
 FT CONFLICT 246 246 N -> D (IN REF. 5).
 FT CONFLICT 256 256 E -> G (IN REF. 5).
 FT CONFLICT 260 260 N -> D (IN REF. 5).
 FT CONFLICT 266 266 N -> D (IN REF. 5).
 FT CONFLICT 280 280 Y -> W (IN REF. 5).
 FT CONFLICT 284 284 N -> S (IN REF. 5).
 SQ SEQUENCE 323 AA; 35404 MW; 69E8A118D579A8B CRC64;
 Query Match 70.1%; Score 883; DB 1; Length 323;
 Best Local Similarity 64.5%; Pred. No. 1.4e-65;
 Matches 160; Conservative 34; Mismatches 38; Indels 16; Gaps 2;
 QY 1 EPKSCDKTH-----TC--PPCAPPELLGSPVFLPPPKDKTLMISRTPEV 44
 : : : : : | | | | |

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Db      76 QPVTCAHAPATNTKVDKTVAPSTCSKPTCPPELGLGSPSVFIFFPKPKDTLMSRTPEV 135
Qy      45 TCVVVDVSHEDPEVKFMWYVDGVEVHNKTKPREEOYNSTRVSVLTVLHQNMMNGKEY 104
Db      136 TCVVVDVSDDDPEVQFTWYINNEQVRRAPRLRQEQNSTLRVSTLPLTHQDLRGEEF 195
Qy      105 KCKVNNKALPAPITKTSKAKVQREPOVYTLPPSRDELTRKNQVSLTCLVKGFFPSDIAV 164
Db      196 KCKVNNKALPAPITKTSKAKVQREPOVYTLPPSRDELTRKNQVSLTCLVKGFFPSDIAV 255
Qy      165 EMESNGQPPENNYKTTPTPLVDVSGSFPLYSKLTVDKSRMOQGNVSCSYMHGALNNHYOOR 224
Db      256 EMENKGAEDNYKTTPTPLVDVSGSFPLYSKLTVDKSRMOQGNVSCSYMHGALNNHYOOR 315
Qy      225 SLSSPSCK 232
Db      316 SISRSPPCK 323

RESULT 6
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE I9 gamma-2 chain C region.
OC Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_Taxid=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RA Birstein B.K., Hussain Q.Z., Cedra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RA MEDLINE=71058471; PubMed=5538606;
RN [4]
RP MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cedra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanoen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RA MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cedra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RA MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cedra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC *- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.

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DR PIR; A02151; G2GP.
DR HSSP; P01842; 7EAB.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003597; I9_c1.
DR InterPro; IPR003600; I9_1like.
DR Pfam; PF00047; I9_2.
DR SMART; SM00410; I9_1like; 1.
DR SMART; SM00407; I9_1like; 2.
DR PROSITE; PS00290; I9_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202 N-LINKED (GLCNAC. . .).
FT CARBOHYD 178 178
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 68.1%; Score 858; DB 1; Length 329;
Best Local Similarity 67.4%; Pred. No. 1.6e-63;
Matches 157; Conservative 28; Mismatches 42; Indels 6; Gaps 2;

Qy 1 EPKSCDKTHPCPCPAPELLGDSVFLFPPKPKDTLMSRTPEYTCVVVDVSHEDPEVKF 60
Db 101 ZPBPC---TCPKCPPEINIGSPVFIFPPKPKDTLMSITLPRVTCVVVDVSDDEPEVQF 156
Qy 61 NMWYDGVGVNHNKTKPREEOYNSTRVSVLTVLHQNMMNGKEYKCKVNNKALPAPITEKT 120
Db 157 TWFDVNNKPVGNAETKPREVQNTTFRVESVLPLOHOMLKKKEKCKVNNKALPAPITEKT 216
Qy 121 ISKAKVQREPOVYTLPPSRDELTRKNQVSLTCLVKGFFPSDIAVEMESNGQP--ENNYKT 178
Db 217 ISKTKGAPRMPDVTYTLPPSRDELTRKNQVSLTCLVKGFFPSDIAVEMESNGQP--ENNYKT 276
Qy 179 TPPVLDSVGSFPLYSKLTVDKSRMOQGNVSCSYMHGALNNHYOQSLSPG 231
Db 277 TPPLEDADGVFLYSKLTVDKSRMOQGNVSCSYMHGALNNHYOQSLSPG 329

RESULT 7
GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE I9 gamma-2B chain C region.
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=101116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR HSSP; P01842; 7EAB.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003597; I9_c1.
DR InterPro; IPR003600; I9_1like.
DR Pfam; PF00047; I9_3.
DR SMART; SM00410; I9_1like; 1.
DR SMART; SM00407; I9_1like; 2.
DR PROSITE; PS00290; I9_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80

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FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA: 36497 MW: 55F8B64D48D460A6 CRC64:

Query Match
Best Local Similarity 64.5%; Score 813; DB 1; Length 333;
Matches 145; Conservative 34; Mismatches 49; Indels 0; Gaps 0;

OY 5 CDKHTPCPCPAPELLGGPSVFLPPPKPKDLMISRTPEVYCVVDVSHEDPEVKNYV 64
DB CPTGCTCHKCPVPELLGGPSVFIPEPKPKDILLISQNKVTCVVDVSEEDPDQFSMFV 165
OY 65 DGEVHNKTKPREQYNSTRVSVLTVLHQNMMNGEKYCKVSNKALPAPIETKISK 124
DB 166 NNVEVHTAQTPREQYNSTRVSVLPIQHODMWSGKEFKCKVNNKALPAPIETKISK 225
OY 125 KVQPREQVYTLPPSRDELTKNOVSLTCLVKGFEVSDIAVEMESNGQDENNYKTPPVLD 184
DB 226 KGLVKKPQVYVWGPPTEQTEVSLTCLTSGFLPNDIGEVNTSGHIEKNYKNTPEVMD 285
OY 185 SVGSFELYSKLTVDKSRMOQGNVFCSVMHALNHHYOORSLSPK 232
DB 286 SDGSFMYSKLNVERSRWDSPAFVCSVYHGLNHHHEKSIISRPK 333

RESULT 8
GC3M_MOUSE STANDARD: PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine Ig3 constant region gene.";
RT EMBO J. 3:2041-2046(1984).
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CC -----
CC EMBL: J00451; -; NOT_ANNOTATED_CDS.
CC PIR: B02156; G3MGC.
CC HSSP: P01857; 1FC1.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003597; Ig_C1.
CC InterPro: IPR003600; Ig_Like.
CC Pfam: PF00047; Ig_3.
CC SMART: SM00407; IG1.2.
CC SMART: SM00410; IG_Like; 1.
CC PROSITE: PS00290; IG_MHC; 1.
CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
CC Transmembrane; Alternative splicing.
CC NON_TER 1 1
FT DOMAIN 98 97 CH1.
FT DOMAIN 114 113 HINGE.
FT DOMAIN 223 223 CH2.

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FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA: 36228 MW: F45827174182BAD6 CRC64:

Query Match
Best Local Similarity 64.5%; Score 812.5; DB 1; Length 329;
Matches 145; Conservative 35; Mismatches 41; Indels 3; Gaps 1;

OY 12 PP--CPAPELLGGPSVFLPPPKPKDLMISRTPEVYCVVDVSHEDPEVKNYV 68
DB 106 PPGSSCPGPNLTGGPSVFIPEPKPKDLMISRTKYTCVVDVSEDDPDVHSMFVNKE 165
OY 69 VHNKTKPREQYNSTRVSVLTVLHQNMMNGEKYCKVSNKALPAPIETKISKARVQ 128
DB 166 VHTAMTQPREAQYNSTRVSVLPIQHODMWSGKEFKCKVNNKALPAPIETKISKGRA 225
OY 129 REPQYTLPPSRDELTKNOVSLTCLVKGFEVSDIAVEMESNGQDENNYKTPPVLDVGS 188
DB 226 QTPQYTLPPREQYNSKRVSLTCLVTFSEALISWEERNGELEDYKNTPIILSDGT 285
OY 189 FFELYSKLTVDKSRMOQGNVFCSVMHALNHHYOORSLSPK 232
DB 286 YFLYSKLTVDKSLTVDSMLQGEIFTCVYHGLNHHHTQKNLSRSPK 329

RESULT 9
GC3M_MOUSE STANDARD: PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine Ig3 constant region gene.";
RT EMBO J. 3:2041-2046(1984).
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00451; AAB59655.1; -;
CC EMBL: V01526; CAA24767.1; ALT_SEQ.
CC PIR: A02155; G3MGM.
CC HSSP: P01857; 1FC1.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003597; Ig_C1.
CC InterPro: IPR003600; Ig_Like.
CC Pfam: PF00047; Ig_3.
CC SMART: SM00407; IG1.2.
CC SMART: SM00410; IG_Like; 1.
CC PROSITE: PS00290; IG_MHC; 1.
CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
CC Transmembrane; Alternative splicing.
CC KW

```

| Query Match | Best Local Similarity | Score | DB 1 | Length | 398 |
|---|--|--|-----------|------------------|--------|
| Matches 143; Conservative 35; Mismatches 41; Indels 3; Gaps 1 | 64.4%; | Pred. No. 8.9e-59; | | | |
| SO | SEQUENCE | 398 AA; | 43929 MW; | CEFF264B50A41B95 | CRC64; |
| QY | 12 | PP---CAPELLGGPSVFLPFPKPRDLMISRTPEVTCVVVDYSHEDPEVKFNKVDGVE | 68 | | |
| Db | 106 | PGSSCGPGLNLGGSPVIFPPPKPRKDALMISLTPEKTVVVDVSDDDVHVSWEFVNKE | 165 | | |
| QY | 69 | VHNVKTRPREBOYNSTYRVVSVLTVLHOMNMGKCKVKSNKALPAPIETKISKAKYOP | 128 | | |
| Db | 166 | VHTAMTQPREAQYNSTPEFVVSALPILQDDMMKRGKFKCKVNNKALPAPIETKISKAKRA | 225 | | |
| QY | 129 | REPOVYTLPEPRDELTKAQVSLTCLVYKGFYPSDIADVEMESNGQPPNNKTKTPPVIDS | 188 | | |
| Db | 226 | QTPQVYTIPEPREQMSKKRVSLTCLVTFNFSEALISVEMERGELEIDQYKNTPPIDSDGT | 285 | | |
| QY | 189 | FFLXSKLTVDKSRMOQGVFCGSVWHEALHNNHQQRSLSLSP | 230 | | |
| Db | 286 | YFLXSKLTVDTSNMLQGEIFCSYVHEALHNNHQQKNSRSP | 327 | | |
| RESULT 10 | | | | | |
| GCL_MOUSE | | | | | |
| AC | P01868: | STANDARD; | PRT; | 324 | AA. |
| ID | 21-JUL-1986 (Rel. 01, Created) | | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | | |
| DT | 30-MAY-2000 (Rel. 39, Last annotation update) | | | | |
| DE | Ig gamma-1 chain C region. | | | | |
| OS | Mus musculus (Mouse). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | |
| OX | NCBI_TaxID=10090; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=80045036; PubMed=115953; | | | | |
| RA | Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., | | | | |
| RA | Takahashi N., Mano Y.; | | | | |
| RT | "Cloning and complete nucleotide sequence of mouse immunoglobulin | | | | |
| RL | gamma 1 chain gene."; | | | | |
| RL | Cell 18:559-568(1979). | | | | |
| RP | [2] | | | | |
| RP | SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C). | | | | |
| RX | MEDLINE=80202559; PubMed=6769752; | | | | |
| RA | Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., | | | | |
| RA | Mano Y., Seimann J.G., Peterlin B.M., Leder P., Honjo T.; | | | | |
| RT | "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences | | | | |
| RL | cloned in a bacterial plasmid."; | | | | |
| RL | gene 9:87-97(1980). | | | | |
| RN | [3] | | | | |
| RP | SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21). | | | | |
| RX | MEDLINE=80012837; PubMed=113776; | | | | |
| RA | Rogers J., Clarke P., Salsner W.; | | | | |
| RT | "Sequence analysis of cloned cDNA encoding part of an immunoglobulin | | | | |
| RL | heavy chain."; | | | | |
| RL | Nucleic Acids Res. 6:3305-3321(1979). | | | | |
| RN | [4] | | | | |
| RP | SEQUENCE (MYELOMA PROTEIN MOPC 21). | | | | |
| RX | MEDLINE=78242288; PubMed=98524; | | | | |
| RA | Adetunbo K.; | | | | |
| RT | "Evolution of immunoglobulin subclasses. Primary structure of a | | | | |

| Query Match | Best Local Similarity | Score | DB 1 | Length | 324 |
|--------------|--|--------------------|-----------|---------|-----|
| Matches 136; | Conservative 58.4%; | Pred. No. 6.7e-58; | Indels 9; | Gaps 3; | |
| 2 | PKSCDKHTKPP--CPAPELLGGSVLFPKPKRDTLMISTRPETCVYDVSHEDDEYK | 59 | | | |
| 99 | PROGCG---CKPCTCTVPEV---SSVETFPKPKPDVLTITLTPVTCVVDISKDDPEVQ | 151 | | | |
| 60 | FNNVVDVEVHNHNTKPREDOYNTSVRVSVLTGLHONMMNGKREYKCKVSKNALPAPLEK | 119 | | | |
| 152 | FSMWVDVEVHNHNTKPREDOYNTSVRVSVLTGLHONMMNGKREYKCKVSKNALPAPLEK | 211 | | | |
| 120 | TISKAKVQPREPOVYTLTPSRDELTKNOVSLTCLVKGFPVPSDIAVEMESNGOPENNYKTT | 179 | | | |
| 212 | TISKTKGRKPRAPQVYTLTPSRDELTKNOVSLTCLVKGFPVPSDIAVEMESNGOPENNYKTT | 271 | | | |
| 180 | PVIVDSVSGFEFLSKLVDSKRMQGVGSVWHEGLHNNHYOORSLSLSPGK | 232 | | | |
| 272 | OPTININGSTFYVSKLVNWKSNMEAGITFCVSGHGLHNNHYOORSLSLSPGK | 324 | | | |

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RESULT 11
GCL_RAT STANDARD: PRT: 326 AA.
AC P20759:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Bruggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR: PS0017; PS0017.
DR HSSP: P01842; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR Pfam: PF000407; Ig_3.
DR SMART: SM00407; Igcl.2.
DR PROSITE: PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHD 176 176
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;
N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 62.3%; Score 784.5; DB 1; Length 326;
Best Local Similarity 58.5%; Pred. No. 1.7e-57;
Matches 137; Conservative 46; Mismatches 42; Indels 9; Gaps 3;

QY 2 PKSCDKTHRCPPCAPPELLG--PSVFLFPKPKDTLMISRTPEVTCVVVSHDEPV 58
DB 99 PRNCG--GDCKPC-----ICTGSEVSSVFLFPKPKDVLTLTLFVTCVVVDISODDEPV 152
QY 59 KENWYVDGEVHNVTKPREQYNSTYRVSVLTVLHOMWANGKEKCKVSKALPAPIE 118
DB 153 HSWVEVDVEHTAQTREPEQNSFRVSSELPILHOMWANGRFRCKVTAAPSPPIE 212
QY 119 KTIKAKVQPREPOVYITLPSRDELTKNOVSLTCLVKGYPDIADVEMSNQPENNKT 178
DB 213 KTIKSPREGTQVPHYITSPKEMTQNEVSITCMVKGYPDIADVEMSNQPENNKT 272
QY 179 TPPEVDSVGSFPLYSKLVFVDRKRMQGNVFNESVMEALHNHYOORSLSLSPGK 232
DB 273 TPPEVDSVGSFPLYSKLVFVDRKRMQGNVFNESVMEALHNHYOORSLSLSPGK 326

RESULT 12
GCL_MOUSE STANDARD: PRT: 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
RT conserved transmembrane sequence and a 28-residue intracellular
RT domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
RT immunoglobulin gamma chains.";
RL Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=82222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -! ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC SEGMENT OF MU CHAINS.
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CC -----
DB EMBL: V00793; CAA24172.1; -
DB EMBL: V00793; CAA24173.1; -
DB EMBL: V00793; CAA24174.1; -
DB PIR: B02159; G1MSM.
DB HSSP: P01842; 7FAB.
DB MGD: MGI:96446; IgH-4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR Pfam: PF000407; Ig_3.
DR SMART: SM00407; Igcl.2.
DR PROSITE: PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1 1
FT DOMAIN 98 97 CH1.
FT DOMAIN 111 110 HINGE.
FT DOMAIN 113 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHD 174 174
FT DISULFID 244 302
N-LINKED (GLCNAC. . .)

```

| FT | TRANSMEM | 340 | 357 | POTENTIAL. |
|---------------------------|--|--|--------------------|----------------------------------|
| FT | DOMAIN | 358 | 393 | CYTOPLASMIC (POTENTIAL). |
| SO | SEQUENCE | 393 AA; | 43386 MW; | 4CC088343B7A1CE27 CRC64; |
| Query Match | | | | |
| Best Local Similarity | | 62.3%; | Score 784.5; | DB 1; Length 393; |
| Matches 135; Conservative | | 58.2%; | Pred. No. 2.2e-57; | |
| | | 47; | Mismatches 41; | Indels 9; Gaps 3; |
| QY | 2 | PKSCDKHTPCPP--CPAPELLGGGVSFLFPKPKQDTLISRPEVTCVAVDVSHEDPEVK | 59 | |
| Dd | 99 | PRDGG-----CKPCLCTYPEV---SSVLFEPKPKDVLITTLTPKTCVAVDISKDDPEVQ | 151 | |
| QY | 60 | FNMYVDGEVHNVYKTRPREEOYNSTYRVSVLYVLHQNMNGKEKCYKSVNKALPAPIEK | 119 | |
| Dd | 152 | FSMFVDDVEVHTAQTQPREEOFNSTFRVSSELPILHMDLNGKEKCYKSVNKAAPAPIEK | 211 | |
| QY | 120 | TISAKAYQRRPQRYVLTTPSRDELTKFNQVSLTCLVKGKSPGPDIANEMVSNQOPENNYKTT | 179 | |
| Dd | 212 | TISTKGGPKPKAPQYTTTTPPKQMKDKVSLTCLMTDFPEDTLYEWMNQPAENYKNT | 271 | |
| QY | 180 | PPVLDVSGSFPLYSKLTLYDKSRMOQGNFSCSVMEHDLAHNHYOQKSLSLSPG | 231 | |
| Dd | 272 | QPIWNTGSGYVYVSKLVNQKSNWEAGNFTGCSVLHEGJLHNNHTKSLSHSG | 323 | |
| RESULT 13 | | | | |
| GC | GC_RAT | STANDARD; | PRT; | 329 AA. |
| AC | P20762; | | | |
| DT | 01-FEB-1991 (Rel. 17, Created) | | | |
| DT | 01-FEB-1991 (Rel. 17, Last sequence update) | | | |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update) | | | |
| DE | 19 gamma-2C chain C region. | | | |
| OS | Rattus norvegicus (Rat). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OX | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | | | |
| NCBI | Taxid:10116; | | | |
| RP | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE:88166903; PubMed-3127222; | | | |
| RA | Burgemann M., Delmastro-Galfrè P., Waldmann H., Calabi F.; | | | |
| RT | "Sequence of a rat immunoglobulin gamma 2C heavy chain constant | | | |
| RT | region cDNA: extensive homology to mouse gamma 3," | | | |
| RL | Eur. J. Immunol. 18:317-319(1988). | | | |
| CC | ----- | | | |
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| CC | entities requires a license agreement (See http://www.isb-sib.ch/announce/ | | | |
| CC | or send an email to license@isb-sib.ch). | | | |
| CC | ----- | | | |
| DR | EMBL; X07189; CAA30169.1; - | | | |
| DR | PIR; S00847; S00847. | | | |
| DR | HSP; P01842; 7EAB. | | | |
| DR | InterPro: IPR003006; Ig_MHC. | | | |
| DR | InterPro: IPR003597; Ig_c1. | | | |
| DR | InterPro: IPR003600; Ig_like. | | | |
| DR | Pfam; PF0004; Ig; 2. | | | |
| DR | SMART; SM00410; Ig_like; 1. | | | |
| DR | SMART; SM00407; Igcl; 2. | | | |
| DR | PROSITE; PS00290; IG_MHC; 1. | | | |
| KW | Immunoglobulin domain; Immunoglobulin C region. | | | |
| FT | NON_TER | 1 | | |
| FT | DOMAIN | 1 | 97 | CH1. |
| FT | DOMAIN | 98 | 113 | HINGE. |
| FT | DOMAIN | 114 | 222 | CH2. |
| FT | DOMAIN | 223 | 329 | CH3. |
| FT | DISULEID | 15 | 15 | INTERCHAIN (WITH A LIGHT CHAIN). |
| FT | DISULEID | 27 | 82 | INTERCHAIN (WITH A HEAVY CHAIN). |
| FT | DISULEID | 111 | 111 | INTERCHAIN (WITH A HEAVY CHAIN). |
| FT | DISULEID | 113 | 113 | INTERCHAIN (WITH A HEAVY CHAIN). |

| FT | DISULFID | 143 | 203 | |
|-----------|---|---|------------------|--------------------------------|
| FT | DISULFID | 249 | 307 | |
| SO | SEQUENCE | 329 AA; | 36571 MW; | 5FCD/B7933850773 CRC64; |
| | Query Match | | 61.6%; | Score 776.5; DB 1; Length 329; |
| | Best Local Similarity | 61.6%; | Pred. No. 8e-57; | |
| | Matches 138; | Conservative 42; | Mismatches 41; | Indels 3; Gaps |
| QY | 12 | PC---CAPELLGSPVFLRPKPKDLMISRPEVYCVVVDVSHDEPKFMVYDGV | | |
| DB | 106 | PPTDICKDDDLGRSPVFLRPKPKDLMITLTPKVCVVVDVSEEDPDQFSMFVDNFR | | |
| QY | 69 | VHNATKPREQVNSTRVVSVLVTLHQNMMNGKEYKCKSNALPAPIEKITSKAKVOF | | |
| DB | 166 | VETQOTQPHEDQNGTRFVAVSTLHIGQDMMSCKEFCVKNNDLDSPIEKITSKRGKAK | | |
| QY | 129 | REPVYTLPPSRDELTLNQNVSFLCLVNGGFPSDIAVEMESNGCPENNYKTPPVLDVS | | |
| DB | 226 | RTPVYTLIPPRPEQMSKNKSLTCMVTSFYPAISVEMENGELEDQKNTLFLVLDSE | | |
| QY | 189 | FFLYSKLTVDSKRMQGNVSCSMYHAFALNNHYQQRSLSPK 232 | | |
| DB | 286 | YFLYSKLSVDTDSMNRDITCSVYHAFALNNHHTQKLSLSPK 329 | | |
| RESULT 14 | | | | |
| | GCAA_MOUSE | STANDARD; | PRT; | 330 AA. |
| ID | GCAA_MOUSE | | | |
| AC | P01863; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| DT | 30-MAY-2000 (Rel. 39, Last annotation update) | | | |
| DE | 1g gamma-2A chain C region, A allele. | | | |
| OC | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=81076554; PubMed=6777755; | | | |
| RA | Sikorav J.-L., Auffray C., Rougeon F.; | | | |
| RT | "Structure of the constant and 3' untranslated regions of the murine | | | |
| RT | Balb/c gamma 2a heavy chain messenger RNA." | | | |
| RL | Nucleic Acids Res. 8:3143-3155(1980). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=81198976; PubMed=6262729; | | | |
| RA | Yamawaki-Katoka Y., Miyata T., Honjo T.; | | | |
| RT | "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene | | | |
| RT | and evolution of heavy chain genes: further evidence for intervening | | | |
| RT | sequence-mediated domain transfer." | | | |
| RL | Nucleic Acids Res. 9:1365-1381(1981). | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=81223894; PubMed=6787604; | | | |
| RA | Olio R., Auffray C., Morchamps C., Rougeon F.; | | | |
| RT | "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes | | | |
| RT | suggests that exons can be exchanged between genes in a multigenic | | | |
| RT | family." | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981). | | | |
| RN | [4] | | | |
| RP | MYELOMA PROTEIN MOPC 173. | | | |
| RX | MEDLINE=74175517; PubMed=4831970; | | | |
| RA | Bourgeois A., Fougereau M., Rocca-Serra J.; | | | |
| RT | "Determination of the primary structure of a mouse IgG2a | | | |
| RT | immunoglobulin: amino-acid sequence of the Fc fragment. Implications | | | |
| RT | for the evolution of immunoglobulin structure and function." | | | |
| RL | Eur. J. Biochem. 43:423-435(1974). | | | |
| RN | [5] | | | |
| RP | DISULFIDE BONDS. | | | |
| RX | MEDLINE=73056887; PubMed=4565406; | | | |
| RA | De Preval C., Fougereau M.; | | | |
| RT | "Determination of the primary structure of a mouse gamma G2a | | | |

RT Immunoglobulin. Identification of the disulfide bridges."
RL Eur. J. Biochem. 30:452-462(1972).
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DR EMBL; V00798; CAA24178.1; -.
DR PIR; A02152; GZMSA.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_1like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00410; Ig_1like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
KW NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;
REMOVED POST-TRANSLATIONALLY.
Query Match 61.6%; Score 776; DB 1; Length 330;
Best Local Similarity 62.9%; Pred. No. 8.9e-57;
Matches 141; Conservative 31; Mismatches 50; Indels 2; Gaps 1;
QY 11 CPE--CPAPELLGSPVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNYDQVE 68
DB 107 CPKCPAPNLLGGPSVFIFPPKIKDVLMISSLPIVTCVVVDVSHEDDPDQVQISMFVNVE 166
QY 69 VHNKTKPREQYNSYRVVSVLVTHQNMNNGKEVCKKVSNNKALPAPIEKTISKAKVQ 128
DB 167 VHTAQTQTHREDYNSLTLLVVSALPIQHDWMSGKEFKCKVKNNKDLPAPIERTISKPSGV 226
QY 129 REPQVYTLPRSRDELTKNOVSLTCLVKGFPYSDIAVEENSGQPENNYKTPPVLDSDGS 188
DB 227 RAPQVYTLPRPEEETKQVTLTCVYTPMPEDIVETNNGKTELNTKNTPEVLDSOGS 286
QY 189 FFLYSKLTVDKSRMQGNVFCQSYMHGALNNHYQORSLSLSPGK 232
DB 287 YFWSKSLRVEKKNNWERNYSQSYVHEGLHNHTTKSRTPGK 330
RESULT 15
GCAB_MOUSE STANDARD; PRT; 335 AA.
ID GCAB_MOUSE
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2a chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037777; PubMed=6794027;
RA Dojini M.O., Lauwereys M., Stroosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain Fc regions of Ig1a and Ig1b allotypic forms."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -1- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS:
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CC -----
DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; GZMSAB.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_1like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_1like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
KW NON_TER 1 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN 12
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dojini M.O., Lauwereys M., Stroosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain Fc regions of Ig1a and Ig1b allotypic forms."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -1- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS:
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CC -----
DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; GZMSAB.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_1like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_1like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
KW NON_TER 1 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
Query Match 61.3%; Score 772; DB 1; Length 335;
Best Local Similarity 60.1%; Pred. No. 1.9e-56;
Matches 137; Conservative 39; Mismatches 52; Indels 0; Gaps 0;
QY 5 CDKTHCPAPELLGSPVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNY 64
DB 108 CPKCPAPNLLGGPSVFIFPPKIKDVLMISSLPIVTCVVVDVSHEDDPDQVQISMFVNVE 167
QY 65 DGEVHNKTKPREQYNSYRVVSVLVTHQNMNNGKEVCKKVSNNKALPAPIEKTISKAKV 124
DB 168 NVEVHTAQTQTHREDYNSLTLLVVSALPIQHDWMSGKEFKCKVKNNKDLPAPIERTISKPS 227
QY 125 KQPREQVYTLPRSRDELTKNOVSLTCLVKGFPYSDIAVEENSGQPENNYKTPPVLD 184
DB 228 RAPQVYTLPRPEEETKQVTLTCVYTPMPEDIVETNNGKTELNTKNTPEVLDSOGS 287
QY 185 SVGSFFLYSKLTVDKSRMQGNVFCQSYMHGALNNHYQORSLSLSPGK 232
DB 288 SGGSYFWSKSLRVEKKNNWERNYSQSYVHEGLHNHTTKSRTPGK 335

Search completed: July 15, 2003, 06:58:19
Job time : 8.24353 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:54:24 ; Search time 26.0767 Seconds
(without alignments)
1833.165 Million cell updates/sec

Title: US-09-847-208b-3
Perfect score: 1260
Sequence: 1 EPKSCDKHTHTCPAPAPPELL.....MHDLNHNHQQRSLSLSPGK 232

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query length | ID | Description |
|------------|-------|--------------|----------------|---------------------|
| 1 | 1225 | 97.2 | 471 4 Q8TC77 | Q8TC77 homo sapien |
| 2 | 1225 | 97.2 | 701 4 Q96P08 | Q96P08 homo sapien |
| 3 | 1097 | 87.1 | 473 4 Q8TC63 | Q8TC63 homo sapien |
| 4 | 877.5 | 69.6 | 337 6 Q95M34 | Q95M34 equus caball |
| 5 | 798.5 | 63.4 | 469 11 Q8R3V9 | Q8R3V9 mus musculu |
| 6 | 795.5 | 63.1 | 463 11 Q991C4 | Q991C4 mus musculu |
| 7 | 791.5 | 62.8 | 437 11 Q9R1A4 | Q9R1A4 mus musculu |
| 8 | 782 | 62.1 | 473 11 Q9D8L4 | Q9D8L4 mus musculu |
| 9 | 772 | 61.3 | 468 11 Q991J1 | Q991J1 mus musculu |
| 10 | 772 | 61.3 | 473 11 Q991J25 | Q991J25 mus musculu |
| 11 | 752.5 | 59.7 | 473 11 Q91205 | Q91205 mus musculu |
| 12 | 752.5 | 59.7 | 474 11 Q8R3H6 | Q8R3H6 mus musculu |
| 13 | 347 | 27.5 | 375 4 Q9BS21 | Q9BS21 homo sapien |
| 14 | 347 | 27.5 | 597 4 Q9BOB8 | Q9BOB8 homo sapien |
| 15 | 347 | 27.5 | 597 4 Q9BB89 | Q9BB89 homo sapien |
| 16 | 347 | 27.5 | 597 4 Q9BU10 | Q9BU10 homo sapien |

| | | | | |
|----|-------|------|---------------|--------------------|
| 17 | 343 | 27.2 | 613 11 Q8VCX7 | Q8VCX7 mus musculu |
| 18 | 337 | 26.7 | 588 4 Q8MUX4 | Q8MUX4 homo sapien |
| 19 | 337 | 26.7 | 613 4 Q96EY0 | Q96EY0 homo sapien |
| 20 | 337 | 26.7 | 613 4 Q8WUK1 | Q8WUK1 homo sapien |
| 21 | 337 | 26.7 | 614 4 Q96GA6 | Q96GA6 homo sapien |
| 22 | 337 | 26.7 | 618 4 Q96AA6 | Q96AA6 homo sapien |
| 23 | 272.5 | 21.6 | 684 13 Q90544 | Q90544 ginglymosto |
| 24 | 259 | 20.6 | 486 11 Q91207 | Q91207 mus musculu |
| 25 | 259 | 20.6 | 487 11 Q99KA4 | Q99KA4 mus musculu |
| 26 | 258 | 20.5 | 426 11 Q9PCD9 | Q9PCD9 mus musculu |
| 27 | 251.5 | 20.0 | 481 11 Q91WT3 | Q91WT3 mus musculu |
| 28 | 251.5 | 20.0 | 481 11 Q91WT1 | Q91WT1 mus musculu |
| 29 | 251.5 | 20.0 | 482 11 Q91X92 | Q91X92 mus musculu |
| 30 | 251.5 | 20.0 | 484 11 Q8VEA0 | Q8VEA0 mus musculu |
| 31 | 251.5 | 20.0 | 488 11 Q91WR1 | Q91WR1 mus musculu |
| 32 | 251.5 | 20.0 | 489 11 Q8VCX4 | Q8VCX4 mus musculu |
| 33 | 251 | 19.9 | 384 4 Q9UE60 | Q9UE60 homo sapien |
| 34 | 251 | 19.9 | 494 4 Q96K68 | Q96K68 homo sapien |
| 35 | 251 | 19.9 | 496 4 Q96KX8 | Q96KX8 homo sapien |
| 36 | 249.5 | 19.8 | 479 11 Q91WP5 | Q91WP5 mus musculu |
| 37 | 248.5 | 19.7 | 480 11 Q91XE1 | Q91XE1 mus musculu |
| 38 | 248 | 19.7 | 496 4 Q96DK0 | Q96DK0 homo sapien |
| 39 | 248 | 19.7 | 500 4 Q9BRV0 | Q9BRV0 homo sapien |
| 40 | 247 | 19.6 | 416 4 Q9NPP6 | Q9NPP6 homo sapien |
| 41 | 246 | 19.5 | 497 4 Q8WY24 | Q8WY24 homo sapien |
| 42 | 243.5 | 19.3 | 479 11 Q99M22 | Q99M22 mus musculu |
| 43 | 243.5 | 19.3 | 481 11 Q8VCV5 | Q8VCV5 mus musculu |
| 44 | 243.5 | 19.3 | 484 11 Q99LA6 | Q99LA6 mus musculu |
| 45 | 182.5 | 14.5 | 259 13 Q90530 | Q90530 ginglymosto |

ALIGNMENTS

RESULT 1
ID Q8TC77 PRELIMINARY; PRT; 471 AA.
AC Q8TC77;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAR24289.1;
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF586606 CRC64;

Query Match 97.2%; Score 1225; DB 4; Length 471;

Best Local Similarity 97.0%; Pred. No. 4.8e-108;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | EPKSCDKHTHTCPAPAPPELLAGPSVFLPPPKDITMISRTPEVTCVVVDVSHDDPEYKF | 60 |
| DB | 240 | EPKSCDKHTHTCPAPAPPELLAGPSVFLPPPKDITMISRTPEVTCVVVDVSHDDPEYKF | 299 |
| QY | 61 | NWYVDGVEVHNHAKKRPREDQNSITRYVSIVTILHOMNMNKKYCKYSNKAAPLPIEKT | 120 |
| DB | 300 | NWYVDGVEVHNHAKKRPREDQNSITRYVSIVTILHOMNMNKKYCKYSNKAAPLPIEKT | 359 |
| QY | 121 | ISKAKVQPREPQVYTLPPSRDELTKNOVSLCLVKGFPSPDIAVEMESNGCPENNYKTPP | 180 |
| DB | 360 | ISKAKGPREPQVYTLPPSRDELTKNOVSLCLVKGFPSPDIAVEMESNGCPENNYKTPP | 419 |
| QY | 181 | PVLDSVGSFSLYSKLTVDKSRWQGNVFSQVMHDLNHNHQQRSLSLSPGK | 232 |

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Db      420 PVLDSGSEFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKSLSPGK 471
RESULT 2
ID      096P08      PRELIMINARY;      PRT;      701 AA.
AC      096P08;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE      Factor VII active site mutant immunocjugate.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21477448; PubMed=11593034;
RA      Hu Z., Garen A.;
RT      "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT      cells for immunotherapy in mouse models of prostatic cancer.";
RL      Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR      EMBL; AF272774; AAK58686.1; -.
DR      InterPro: IPR000152; Asx_hydroxyl.
DR      InterPro: IPR000561; EGF-like.
DR      InterPro: IPR000742; EGF-2.
DR      InterPro: IPR001881; EGF_CA.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR001254; Ser_protease_Try.
DR      InterPro: IPR000294; VltK_dep_GLA.
DR      Pfam: PF00008; EGF_2.
DR      Pfam: PF00594; g1a; 1.
DR      Pfam: PF00047; Ig_2.
DR      Pfam: PF00089; trypsin; 1.
DR      SMART; SM00181; EGF_2.
DR      PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR      PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR      PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR      PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR      PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR      PROSITE; PS50240; TRYPSIN_DOM; 1.
DR      PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR      PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW      Hydrolase; Serine protease.
SQ      SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match      97.2%; Score 1225; DB 4; Length 701;
Best Local Similarity 97.0%; Pred. No. 8.2e-108;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 EPPSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
      |||||||
DB      470 EPPSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 529
QY      61 NATYDGEVHNATKPREEQYNSTYRVSVLTLYLHOMMANGKEYKCKVSKALPAPIEKT 120
      |||||||
DB      530 NATYDGEVHNATKPREEQYNSTYRVSVLTLYLHOMMANGKEYKCKVSKALPAPIEKT 569
QY      121 ISRAKVOPEPPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTP 180
      |||||||
DB      590 ISRAKQCPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTP 649
QY      181 PVLDSGSEFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKSLSPGK 232
      |||||||
DB      650 PVLDSGSEFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKSLSPGK 701

RESULT 3
ID      08TC63      PRELIMINARY;      PRT;      473 AA.
AC      08TC63;
DT      01-JUN-2002 (TREMBLrel. 21, Created)

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DT      01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Hypothetical 52.0 kDa protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=KIDNEY;
RA      Strausberg R.;
RL      Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC025985; AAK25985.1; -.
KW      Hypothetical protein.
SQ      SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match      87.1%; Score 1097; DB 4; Length 473;
Best Local Similarity 90.5%; Pred. No. 7.1e-96;
Matches 201; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY      11 CPSPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGYEVH 70
      |||||||
DB      252 CPSPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGYEVH 311
QY      71 NAKTKPREEQYNSTYRVSVLTLYLHOMMANGKEYKCKVSKALPAPIEKTISAKKQPRE 130
      |||||||
DB      312 NAKTKPREEQYNSTYRVSVLTLYLHOMMANGKEYKCKVSKALPAPIEKTISAKKQPRE 371
QY      131 PÖVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPPVLDSGSF 190
      |||||||
DB      372 PÖVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPPVLDSGSF 431
QY      191 LYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKSLSPGK 232
      |||||||
DB      432 LYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKSLSPGK 473

RESULT 4
ID      095M34      PRELIMINARY;      PRT;      337 AA.
AC      095M34;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Immunoglobulin gamma 1 heavy chain constant region
DE      (Fragment).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX      NCBI_TaxID=9796;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Wagner B.;
RL      Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98383416; PubMed=9717671;
RA      Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA      Leibold W., Radbruch A.;
RT      "Organization of the equine immunoglobulin heavy chain constant region
RT      genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL      Immunobiology 199:105-119(1998).
DR      EMBL; AJ300675; CAC44624.1; -.
DR      InterPro: IPR003006; Ig_MHC.
DR      Pfam: PF00047; Ig_2.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT      NON TER
FT      1
SQ      SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match      69.6%; Score 877.5; DB 6; Length 337;
Best Local Similarity 67.7%; Pred. No. 3.3e-75;
Matches 157; Conservative 36; Mismatches 36; Indels 3; Gaps 2;

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| QY | 3 | KSCQKTHQPCPCAPPELLGGGSVLP.PPKPKDITLMSPTPVCVVVDVSHEDPEVK | 62 |
|--|--|---|---------------------------|
| | 107 | KVCDMS-KCRKCPAPPELLGGGSVLP.PPKPKDITLMSPTPVCVVVDVSHEDPEVK <td>165</td> | 165 |
| QY | 63 | VYDGEVHNATKPREEOYNSTYRVSVLYLHONMMNGKRYCKGKVSNAKLPADIEKTS <td>122</td> | 122 |
| | 166 | YMDGEVRYLATRKEQDFNSTYRVSVLYLRQHDWLISGKRFCKKVNQALPPIERIT <td>225</td> | 225 |
| QY | 123 | KAKQAPPEPOVYITLPSSHDELTKNOVSLTCLVKGFPYSDIAVEMESNGQP--ENNYKTP <td>180</td> | 180 |
| | 226 | KTGRSGEPQVYVLAIPHDELKSKSVSTCLVKGFPYSDIAVEMESNGQPLELETKYSTQ <td>285</td> | 285 |
| QY | 181 | PVLDVSFSFLYSKLTVDKSRMOQGNFSCSVMEHALHNHQSLSPK <td>232</td> | 232 |
| | 286 | AQDDSGSYFLYSKLTVDKSRMOQGNFSCSVMEHALHNHQSLSPK <td>337</td> | 337 |
| RESULT 5 | | | |
| Q8R3V9 | ID | Q8R3V9 | PRELIMINARY: PRT: 469 AA. |
| AC | Q8R3V9 | 01-JUN-2002 (TREMBLrel. 21, Created) | |
| DT | 01-JUN-2002 (TREMBLrel. 21, Last sequence update) | | |
| DT | 01-JUN-2002 (TREMBLrel. 21, Last annotation update) | | |
| DE | Hypothetical 52.0 kDa protein. | | |
| OS | Mus musculus (Mouse). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| OX | NCBI_TaxID=10090; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Strausberg R.; | | |
| RL | Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases. | | |
| DR | EMBL; BC024405; AAH24405.1; - | | |
| SW | Hypothetical protein. | | |
| SEQ | SEQUENCE 469 AA; 51976 MW; 534793f155D05457 CRC64; | | |
| Query Match 63.4%; Score 798.5; DB 11; Length 469; | | | |
| Best Local Similarity 59.2%; Pred. No. 1.6e-67; | | | |
| Matches 138; Conservative 45; Mismatches 41; Indels 9; Gaps 3. | | | |
| QY | 2 | PKSCDKTHHTCPP--CPAPPELLGGGSVLP.PPKPKDITLMSPTPVCVVVDVSHEDPEVK | 59 |
| | 244 | PRDGG---CKRCICTVPEV---SSVLFPPKPKDVLITLTPKVTQVVVDISKDPEVQ | 296 |
| QY | 60 | FNMTYDGEVHNATKPREEOYNSTYRVSVLYLHONMMNGKRYCKGKVSNAKLPADIEK | 119 |
| | 297 | FSMWVDVDEYHTAOTKPREEOFNSTFRVSSELRIMHODMLNGKEFKCVNSAAPPADIEK | 356 |
| QY | 120 | TISAKAPQRRPOVYITLPSSHDELTKNOVSLTCLVKGFPYSDIAVEMESNGQPENNYKTT | 179 |
| | 357 | TISTKTGKPKAPQVYITLPPEQAKDKVSLTCLMTDFPEDITVEMQNGQPAENYKNT | 416 |
| QY | 180 | PVLDVSFSFLYSKLTVDKSRMOQGNFSCSVMEHALHNHQSLSPK | 232 |
| | 417 | QPIMDTGSYVYVSKLTQKSNWEGNFTFCSVLHEGLHNHTKESLSHSPOK | 469 |
| RESULT 6 | | | |
| Q891C4 | ID | Q891C4 | PRELIMINARY: PRT: 463 AA. |
| AC | Q891C4 | 01-JUN-2001 (TREMBLrel. 17, Created) | |
| DT | 01-JUN-2001 (TREMBLrel. 17, Last sequence update) | | |
| DT | 01-JUN-2002 (TREMBLrel. 21, Last annotation update) | | |
| DE | Similar to RIKEN cDNA 1810060009 gene. | | |
| GN | IGH-4. | | |
| OS | Mus musculus (Mouse). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| OX | NCBI_TaxID=10090; | | |
| RN | [1] | | |

[illegible]

RESULT 10
ID Q99L25 PRELIMINARY: PRT: 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to Riken cDNA 181060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AH03888.1; .
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003597; IG.
DR InterPro; IPR003600; IG_c1.
DR InterPro; IPR003006; IG_like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 61.3%; Score 772; DB 11; Length 473;
Best Local Similarity 62.9%; Pred. No. 5.5e-65;
Matches 141; Conservative 31; Mismatches 50; Indels 2; Gaps 1;
QY 11 CPE--CPAPELLGSPVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNNYVDSGE 68
DB 250 CPCKCPAPNLGGPSVFLPPPKIKDVLMLISLPMVTCVVVDVSDDDVDVIGSNVNVVE 309
QY 69 VHNKTKPREEQYNSTYRVSVLTVLHONMNGKEYCKVSNKALPAPIETKISKAVQ 128
DB 310 VLTQOTQTHREDYNSTLRVSALPIQHDWMSGKEFKCKVNNKALPAPIETKISKAVQ 369
QY 129 REPQVYTLPRSDRLTKNQVSLTCLVKGFYPSDIAVEESGQPENNNKTPPVLDSDGS 188
DB 370 RAPQVYTLPRPEEETKQVTLTCVYDEVPEFIDIVETNTNNGKTELKNTPEVLDSDGS 429

RESULT 11
ID Q91Z05 PRELIMINARY: PRT: 473 AA.
AC Q91Z05;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN A0044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; .
DR MGI; MGI:2144967; A0044919.

DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
RW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 59.7%; Score 752.5; DB 11; Length 473;
Best Local Similarity 58.6%; Pred. No. 3.9e-63;
Matches 140; Conservative 36; Mismatches 56; Indels 7; Gaps 2;
QY 1 EPKSCDKT-HTCPP-----CPAPELLGSPVFLPPPKPKDLMISRTPEVTCVVVDVSH 53
DB 235 EPSGPISTINCPCKCKCHKCPAPNLBEGPSVFLPPPKIKVLMISLTPKTKCVVVDVSE 294
DB 295 DDPOVQISWFEVNNVEVHTAQOTQTHREDYNSTLRVSALPIQHDWMSGKEFKCKVNNKDL 354
QY 114 PAPIETKISKAKVQPREQVYTLPRSDRLTKNQVSLTCLVKGFYPSDIAVEESGQPE 173
DB 355 PPIERTSKTKTKGLVRAQVYTLPPPEQLSKVDLSLCLVGFNPGDISVETWSNGHTE 414
QY 174 NNYKTPPVLDVSGSFYLSKLTVDKSRMQGNVSCSVMHGALNNHYOQRLSLSPGK 232
DB 415 ENYKDTAVLDSDGSYFLYSKLDIKTSKWEKTDSPSCVRRHGLKNYLLKTKTISRSPGK 473

RESULT 12
ID Q8R3H6 PRELIMINARY: PRT: 474 AA.
AC Q8R3H6;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 51.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (Mar-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AAH25447.1; .
RW Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 59.7%; Score 752.5; DB 11; Length 474;
Best Local Similarity 58.6%; Pred. No. 3.9e-63;
Matches 140; Conservative 36; Mismatches 56; Indels 7; Gaps 2;

QY 1 EPKSCDKT-HTCPP-----CPAPELLGSPVFLPPPKPKDLMISRTPEVTCVVVDVSH 53
DB 236 EPSGPISTINCPCKCKCHKCPAPNLBEGPSVFLPPPKIKVLMISLTPKTKCVVVDVSE 295
QY 54 EDPVEKFMWYDGVVHNVKTKPREQYNSTYRVSVLTVLHONMNGKEYCKVSNKAL 113
DB 296 DDPOVQISWFEVNNVEVHTAQOTQTHREDYNSTLRVSALPIQHDWMSGKEFKCKVNNKDL 355
QY 114 PAPIETKISKAKVQPREQVYTLPRSDRLTKNQVSLTCLVKGFYPSDIAVEESGQPE 173
DB 356 PPIERTSKTKTKGLVRAQVYTLPPPEQLSKVDLSLCLVGFNPGDISVETWSNGHTE 415
QY 174 NNYKTPPVLDVSGSFYLSKLTVDKSRMQGNVSCSVMHGALNNHYOQRLSLSPGK 232
DB 416 ENYKDTAVLDSDGSYFLYSKLDIKTSKWEKTDSPSCVRRHGLKNYLLKTKTISRSPGK 474

RESULT 13
ID Q9BSZ1 PRELIMINARY: PRT: 375 AA.
AC Q9BSZ1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to Riken cDNA 181060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; .
DR MGI; MGI:2144967; A0044919.

AC Q9BSZ1: 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 41.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH;
RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004476; AAH04476.1; -
DR HSSP; P01857; 1FC1.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00410; Ig-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 375 AA; 41314 MW; B1A0A0998F473619 CRC64;

Query Match 27.5%; Score 347; DB 4; Length 375;
Best Local Similarity 33.6%; Pred. No. 9.8e-25;
Matches 72; Conservative 48; Mismatches 86; Indels 8; Gaps 6;

QY 25 VFLEPPKPKDTLMISRTPEVTCVVDVSHDEPEKFMWYDGVGVHNVKTKPREQYNST 84
DB 146 VFAIPSPS-FASIFLTSTKLTCLVTLDTLTYD-SVTISWTRONGEAVKTHNISESHPNAT 203
QY 85 YRVAVSLTVLHOMNMNGEKYKYNKALPAPIEKTISKAK-VQPREQVYTLPPSRDEL 143
DB 204 FSAVGEASICEDDMNGSERFTCTVTHDLPISPKQTSRKGVALLHRPDVLLPAREQL 263
QY 144 T-KNOVSLTCLVKGFPSPDIIVEMESNGQP--ENNYKTPPVLD--SVGSFELYSKLTVD 198
DB 264 NLRRESATITCLVTVGFSPADVGVOMQOGPLSPEKVTSAPEMPQAPGRYFAHSILTVS 323
QY 199 KSRMOGCVNPGSCVMHEALHNHYQORSLSPGK 232
DB 324 EEMNTGETYTCVVAHFAHPNRYTERTVKSTGK 357

RESULT 14

ID Q9BOB8 PRELIMINARY; PRT; 597 AA.
AC Q9BOB8; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Unknown (protein for MGC:1905) (protein for MGC:1228).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -
DR EMBL; BC001872; AAH01872.1; -
DR HSSP; P01825; 7FAB.
DR InterPro: IPR003599; Ig.

DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig_5.
DR SMART; SM00409; Ig_2.
DR SMART; SM00407; Igcl; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; Ig-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 27.5%; Score 347; DB 4; Length 597;
Best Local Similarity 33.6%; Pred. No. 1.8e-24;
Matches 72; Conservative 48; Mismatches 86; Indels 8; Gaps 6;

QY 25 VFLEPPKPKDTLMISRTPEVTCVVDVSHDEPEKFMWYDGVGVHNVKTKPREQYNST 84
DB 368 VFAIPSPS-FASIFLTSTKLTCLVTLDTLTYD-SVTISWTRONGEAVKTHNISESHPNAT 425
QY 85 YRVAVSLTVLHOMNMNGEKYKYNKALPAPIEKTISKAK-VQPREQVYTLPPSRDEL 143
DB 426 FSAVGEASICEDDMNGSERFTCTVTHDLPISPKQTSRKGVALLHRPDVLLPAREQL 485
QY 144 T-KNOVSLTCLVKGFPSPDIIVEMESNGQP--ENNYKTPPVLD--SVGSFELYSKLTVD 198
DB 486 NLRRESATITCLVTVGFSPADVGVOMQOGPLSPEKVTSAPEMPQAPGRYFAHSILTVS 545
QY 199 KSRMOGCVNPGSCVMHEALHNHYQORSLSPGK 232
DB 546 EEMNTGETYTCVVAHFAHPNRYTERTVKSTGK 579

RESULT 15

ID Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9; 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 65.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-CELL;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1; -
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3ADBECE263D9 CRC64;

Query Match 27.5%; Score 347; DB 4; Length 597;
Best Local Similarity 33.6%; Pred. No. 1.8e-24;
Matches 72; Conservative 48; Mismatches 86; Indels 8; Gaps 6;

QY 25 VFLEPPKPKDTLMISRTPEVTCVVDVSHDEPEKFMWYDGVGVHNVKTKPREQYNST 84
DB 368 VFAIPSPS-FASIFLTSTKLTCLVTLDTLTYD-SVTISWTRONGEAVKTHNISESHPNAT 425
QY 85 YRVAVSLTVLHOMNMNGEKYKYNKALPAPIEKTISKAK-VQPREQVYTLPPSRDEL 143
DB 426 FSAVGEASICEDDMNGSERFTCTVTHDLPISPKQTSRKGVALLHRPDVLLPAREQL 485
QY 144 T-KNOVSLTCLVKGFPSPDIIVEMESNGQP--ENNYKTPPVLD--SVGSFELYSKLTVD 198
DB 486 NLRRESATITCLVTVGFSPADVGVOMQOGPLSPEKVTSAPEMPQAPGRYFAHSILTVS 545

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:46:49 ; Search time 27.3185 seconds
(without alignments)
1131.621 million cell updates/sec

Title: US-09-847-208B-3
Perfect score: 1260
Sequence: 1 EPKSCDKHTHCPCPAPELL.....MHEALHNHYOQRSLSLSPGK 232

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1985.DAT:*
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- 8: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1994.DAT:*
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- 19: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/genescp-emb1/AA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/genescp-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/genescp-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/genescp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1225 | 97.2 | 232 | 18 | AAW26232 |
| 2 | 1225 | 97.2 | 232 | 21 | AAW28690 |
| 3 | 1225 | 97.2 | 232 | 22 | AAV72915 |
| 4 | 1225 | 97.2 | 232 | 22 | AAAB8087 |
| 5 | 1225 | 97.2 | 232 | 23 | AAE15347 |
| 6 | 1225 | 97.2 | 233 | 23 | ABBO9463 |
| 7 | 1225 | 97.2 | 251 | 23 | ABBA1490 |
| 8 | 1225 | 97.2 | 259 | 20 | AAV24154 |
| 9 | 1225 | 97.2 | 287 | 22 | AAAB7590 |
| 10 | 1225 | 97.2 | 329 | 17 | AAAB1806 |

| | | | | | |
|----|------|------|-----|----|-----------|
| 11 | 1225 | 97.2 | 330 | 22 | AAAB04071 |
| 12 | 1225 | 97.2 | 330 | 23 | AAAB1641 |
| 13 | 1225 | 97.2 | 330 | 23 | AAE21960 |
| 14 | 1225 | 97.2 | 330 | 23 | ABBO5736 |
| 15 | 1225 | 97.2 | 330 | 23 | AAW47836 |
| 16 | 1225 | 97.2 | 331 | 21 | AAAY91106 |
| 17 | 1225 | 97.2 | 351 | 14 | AAAR3685 |
| 18 | 1225 | 97.2 | 371 | 10 | AAAP1918 |
| 19 | 1225 | 97.2 | 371 | 10 | AAAP3558 |
| 20 | 1225 | 97.2 | 376 | 19 | AAW60037 |
| 21 | 1225 | 97.2 | 379 | 19 | AAW83962 |
| 22 | 1225 | 97.2 | 379 | 19 | AAW49073 |
| 23 | 1225 | 97.2 | 388 | 23 | ABBO7681 |
| 24 | 1225 | 97.2 | 396 | 18 | AAW18574 |
| 25 | 1225 | 97.2 | 396 | 18 | AAW18575 |
| 26 | 1225 | 97.2 | 400 | 21 | AAV15123 |
| 27 | 1225 | 97.2 | 404 | 23 | AAU97108 |
| 28 | 1225 | 97.2 | 423 | 21 | AAAB28693 |
| 29 | 1225 | 97.2 | 424 | 16 | AAW14764 |
| 30 | 1225 | 97.2 | 424 | 16 | AAW14765 |
| 31 | 1225 | 97.2 | 426 | 21 | AAAB28695 |
| 32 | 1225 | 97.2 | 435 | 13 | AAAB6530 |
| 33 | 1225 | 97.2 | 437 | 18 | AAW10532 |
| 34 | 1225 | 97.2 | 441 | 21 | AAAB28692 |
| 35 | 1225 | 97.2 | 442 | 18 | AAW10550 |
| 36 | 1225 | 97.2 | 445 | 20 | AAV24153 |
| 37 | 1225 | 97.2 | 446 | 17 | AAW05829 |
| 38 | 1225 | 97.2 | 447 | 20 | AAV31669 |
| 39 | 1225 | 97.2 | 448 | 21 | AAAB28694 |
| 40 | 1225 | 97.2 | 448 | 23 | AAW49203 |
| 41 | 1225 | 97.2 | 449 | 14 | AAAR3339 |
| 42 | 1225 | 97.2 | 449 | 19 | AAW49816 |
| 43 | 1225 | 97.2 | 451 | 22 | AAE12715 |
| 44 | 1225 | 97.2 | 451 | 23 | AAAB1014 |
| 45 | 1225 | 97.2 | 452 | 20 | AAV30201 |

ALIGNMENTS

RESULT 1
AAW26232
ID AAW26232 standard; Protein: 232 AA.
XX
AC AAW26232;
XX
DT 16-MAR-1998 (first entry)
XX
DE Human IgG1 hinge/Fc region.
XX
KW Fusion protein: hydrophilic spacer; recombinant; expression system;
KW carboxypeptidase; IgG1, immunoglobulin; hinge region; Fc.
XX
OS Homo sapiens.
XX
PN WO9728272-A1.
XX
PD 07-AUG-1997.
XX
PF 31-JAN-1997; 97WO-US01470.
XX
PR 31-JAN-1996; 96US-0595043.
XX
PA (TECH-) TECHNOLOGENE INC.
XX
PI Sgarlato GD;
XX
DR WPI: 1997-402624/37.
XX
DR N-PSDB: AAT80158.
XX
PT Recombinant protein expression system for fusion protein production
PT - useful for high quantity production of authentic recombinant
PT proteins

Zcytor 10::IgG gam
Human IgG gamma 1
Human death domain
Human immunoglobul
Human Ig-gamma1 he
Human rF-Fc-delta-
Human kappa immuno
Sequence of the 11
linked human IgG
Antigenic peptide
Recombinant human
Recombinant human
MOG-Fc fusion prot
Aggrecanase artifi
Porcine C1A-4-19
Mouse MK61-human I
Fc-huA2P-1 (114-28
Human soluble kit
Fc-muA2P-1 (120-29
Sequence of one ch
Alpha-1-acid glyco
Fc-huA2P-1 (95-281
IgG1 polypeptide.
Bovine LOX-1 extra
Humanised 1D10 ant
Human IgG1 chain C
Fc-muA2P-1 (99-291
Humanised monoclon
Completely humanis
Amino acid sequenc
Human recombinant
B7-related protein
Heavy chain sequen

XX Example 3; Page 133-134; 194pp; English.

A novel recombinant vector has been developed which comprises a nucleotide sequence encoding a fusion protein. The fusion protein comprises three domains joined together in order, from N-terminus to C-terminus, of a first domain comprising a protein of interest, a second domain comprising a hydrophilic spacer and an affinity domain, each domain comprising amino acid residues. The present sequence represents the hinge/PC region of human IgG1, used in example 3 of the present invention. The recombinant vector is used for the production of authentic recombinant proteins of interest. The method of the invention is useful for the expression of fusion proteins capable of isolation by affinity chromatography in pro- or eukaryotic cells. This method allows for the efficient cleavage and generation of authentic proteins of interest that do not contain extraneous (i.e. non-naturally occurring) amino acids.

Sequence 232 AA:

| | | | | |
|---------------------------|-------|--------------------|-----------|-------------|
| Query Match | 97.2% | Score 1225; | DB 18; | Length 232; |
| Best Local Similarity | 97.0% | Pred. No. 2.1e-90; | | |
| Matches 225; Conservative | 3; | Mismatches 4; | Indels 0; | Gaps 0; |

| QY | 1 | EPKSCDKITCPCCAPPELLGGPSVFLPPLPKDTLMISRPETLVGVVSHEDPEVK | 60 |
|----|-----|--|-----|
| QY | 1 | EPKSCDKITCPCCAPPELLGGPSVFLPPLPKDTLMISRPETLVGVVSHEDPEVK <td>60</td> | 60 |
| Db | 1 | EPKSCDKITCPCCAPPELLGGPSVFLPPLPKDTLMISRPETLVGVVSHEDPEVK | 60 |
| QY | 61 | NMYVDGVEVHNKTKPREBOYNSTIRVYSVLTVLHOMMNGEKYCKVSNKALPAPLEKT | 120 |
| QY | 61 | NMYVDGVEVHNKTKPREBOYNSTIRVYSVLTVLHOMMNGEKYCKVSNKALPAPLEKT | 120 |
| Db | 61 | NMYVDGVEVHNKTKPREBOYNSTIRVYSVLTVLHOMMNGEKYCKVSNKALPAPLEKT | 120 |
| QY | 121 | ISKAKQPREPOVYITLPPSRDELIRKNOVSLTCLVKGFPDIAEWESNGQPENNYKTP | 180 |
| QY | 121 | ISKAKQPREPOVYITLPPSRDELIRKNOVSLTCLVKGFPDIAEWESNGQPENNYKTP | 180 |
| Db | 121 | ISKAKQPREPOVYITLPPSRDELIRKNOVSLTCLVKGFPDIAEWESNGQPENNYKTP | 180 |
| QY | 181 | PVLVDGSGFELYSKLTIVDKSRMOQGNVWSCVMEHDLAHNHYQQRSLSLSGK | 232 |
| QY | 181 | PVLVDGSGFELYSKLTIVDKSRMOQGNVWSCVMEHDLAHNHYQQRSLSLSGK | 232 |
| Db | 181 | PVLVDGSGFELYSKLTIVDKSRMOQGNVWSCVMEHDLAHNHYQQRSLSLSGK | 232 |

RESULT 2

| ID | standard; Protein; 232 AA. |
|----------|----------------------------|
| AAB28690 | |

AACB28690;

DT 14-FEB-2001 (first entry)

Human IgGgamma1 hinge, CH2 and CH3 regions.

KM Human; AGP-1; type II transmembrane protein; cytosolic; antiviral
 KM antiinflammatory; hepatotropic; antiatherosclerotic; anti-HIV; HIV
 KM human Immunodeficiency virus; apoptosis; proliferative disorder;
 KM cancer; hepatitis; acquired immunodeficiency syndrome; AIDS;
 KM autoimmune disorder; transplant rejection; cardiovascular disease;
 KM arteriosclerosis; IgGgamma1.

OS Homo sapiens.

PN W0200063253-A1.

PD 26-OCT-2000.

24-MAR-2000; 2000WO-US08004.

PR 16-APR-1999; 99US-0293245.

PA (AMGE-) AMGEN INC.

PI Hsu H, Meng S;

DR WPI; 2000-665240/64

XX Fusion protein of AGP-1 protein and an Fc region, used to treat
PT proliferative disorders, immune disorders, and virally-induced
XX disorders -
PS Claim 2, Fig 1, 93pp; English.

PS Claim 2; Fig 1; 93pp; English.

CC The present sequence was used in the production of ACP-1.
CC fusion proteins. ACP-1 is a type II transmembrane protein. The fusion
CC proteins comprise an Fc immunoglobulin region fused to the N-terminal
CC portion of the ACP-1 protein. The fusion proteins can be used to induce
CC apoptosis in a tissue, and to treat proliferative disorders, immune
CC disorders, or virally-induced disorders. The proliferative disorders
CC include cancers, such as breast, prostate, lung or colon cancer. The
CC viral infections include hepatitis, and acquired immunodeficiency
CC syndrome (AIDS), and the immune disorders may be autoimmune disorders
CC or transplant rejection. Cardiovascular diseases such as arteriosclerosis
CC may also be treated. The ACP-1 containing fusion proteins have increased
CC biological activity compared to the soluble ACP-1 proteins used in
CC prior art therapies.

Sequence 232 AA;

| | | | | |
|---------------------------|--------|---------------------|-----------|-------------|
| Query Match | 97.2%; | Score 1225; | DB 21; | Length 232; |
| Best Local Similarity | 97.0%; | Pred. No. 2, 1e-90; | | |
| Matches 225; Conservative | 3; | Mismatches 4; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|---|-----|
| QY | 1 | EPKSCCKTHTCCPCAPABELLGSPVFLPPPKKCDLMSLRPEYVCVVVDVSHDEPEKFK | 60 |
| Db | 1 | EPKSCCKTHTCCPCAPABELLGSPVFLPPPKKCDLMSLRPEYVCVVVDVSHDEPEKFK | 60 |
| QY | 61 | NMTVDGVEVHNKTKPREQVNSTRYVSVLTVLHQNMMNGKEKCKVSNKALPALEKT | 120 |
| Db | 61 | NMTVDGVEVHNKTKPREQVNSTRYVSVLTVLHQNMMNGKEKCKVSNKALPALEKT | 120 |
| QY | 121 | ISAKKQKPREPQVYLLPSPRDELTKNOVSLTCLVKGFPSDIAYEMESNGCPENNYKTPP | 180 |
| Db | 121 | ISAKKQKPREPQVYLLPSPRDELTKNOVSLTCLVKGFPSDIAYEMESNGCPENNYKTPP | 180 |
| QY | 181 | PVLDVSGSFELYSKLTVDKSRMQGQNNVFSCSYMHAEALNNHQQNSLSLSPGK | 232 |
| Db | 181 | PVLDVSGSFELYSKLTVDKSRMQGQNNVFSCSYMHAEALNNHQQNSLSLSPGK | 232 |

RESULT 3
RAY73915

ID. AAY72915 standard; Protein; 232 AA.

AC AAY72915;
vY

DT 13-JUN-2001 (first entry)
YY

Human partial IgG1 protein comprising hinge, CH2 and CH3 regions.

KM Human; fusion protein; osteoprotegerin; OPg/Fc protein; osteonectin;
 KM therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
 KM hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
 KM osteolytic metastasis; prosthetic loosening; immunoglobulin G1;
 IgG1; periodontal.

Homo sapiens.

PN WO200118203-A1

PD 15-MAR-2001.

PF 18-AUG-2000; 2000WO-US22797.

PR 03-SEP-1999; 99US-0389782.

PA (AMGE-) AMGEN INC.

PI Dunstan CR, Wooden SK, Mann MB;

XX WPI: 2001-244572/25.
 DR Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
 XX by e.g. osteoporosis, Paget's disease and osteomyelitis -
 PT
 CC Claim 3; Fig 1; 119pp; English.
 PS
 XX The patent discloses fusion protein comprising human osteoprotegerin
 CC (OPG) protein fused by linker to human IgG1 Fc portion. OPG negatively
 CC regulates formation of osteoclasts in vitro and in vivo. It blocks
 CC the differentiation of osteoclasts from monocyte or macrophage
 CC precursors and the reabsorption of bone. The OPG-Fc fusion protein
 CC is administered for the treatment of bone loss resulting from
 CC osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia,
 CC osteopenia associated with surgery or steroid administration,
 CC osteonecrosis, bone loss due to rheumatoid arthritis, periodontal
 CC bone loss, osteolytic metastasis and/or prosthetic loosening.
 CC The present sequence is partial human immunoglobulin G (Ig G) 1
 CC protein comprising the hinge and heavy chain constant regions CH2
 CC and CH3.
 CC
 SQ Sequence 232 AA:
 Query Match 97.2%; Score 1225; DB 22; Length 232;
 Best Local Similarity 97.0%; Pred. No. 2.1e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSDCKHTHTPCPCAPAPLLGSPVFLPPPKKOTLMISRPEVTCVAVDVSHDEPEVKF 60
 DB 1 EPKSDCKHTHTPCPCAPAPLLGSPVFLPPPKKOTLMISRPEVTCVAVDVSHDEPEVKF 60
 QY 61 NMVYDGVVHNKTKPREEOYNSTRVAVSVLTVLHQNMMNGKEYCKYCNKALPAPIEKT 120
 DB 61 NMVYDGVVHNKTKPREEOYNSTRVAVSVLTVLHQNMMNGKEYCKYCNKALPAPIEKT 120
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVWESNGOPENNYKTTTP 180
 DB 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVWESNGOPENNYKTTTP 180
 QY 181 PVLDSGSEFLYSKLTVDKSRWQGNVSCSYMHALNNHYOQRSLSPGK 232
 DB 181 PVLDSGSEFLYSKLTVDKSRWQGNVSCSYMHALNNHYOQRSLSPGK 232
 RESULT 4
 AAB80897
 ID AAB80897 standard; protein; 232 AA.
 XX
 AC AAB80897;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Human IgGgamma1 hinge, CH2 and CH3 regions.
 XX
 KW Human; IgGgamma1; anticancer; Antimetastatic; Osteogenic;
 KW lytic bone disease; multiple myeloma; immunoglobulin;
 KW osteosclerotic bone metastasis; OPG; osteoprotegerin;
 KW osteoclast formation inhibition; bone resorption inhibition.
 XX
 OS Homo sapiens.
 XX
 PN WO200117543-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 18-AUG-2000; 2000WO-US22806.
 XX
 PR 03-SEP-1999; 99US-0389545.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Dunstan CR;

XX WPI: 2001-265936/27.
 DR Preventing or treating lytic bone diseases, particularly associated
 XX with cancer or metastasis, by administering an osteoprotegerin
 PT polypeptide -
 CC Disclosure: Fig 1; 87pp; English.
 PS
 XX The present invention relates to a method for the prevention or treatment
 CC of lytic bone disease or multiple myeloma. Also the method can be used
 CC for preventing metastasis of cancer to bone or osteosclerotic bone
 CC metastasis. The method comprises administering an OPG (osteoprotegerin)
 CC polypeptide or OPG fusion protein. The OPG proteins (see
 CC AAB80898-AAB80905) can inhibit formation of osteoclasts (and thus bone
 CC resorption) by blocking differentiation from monocytes/macrophage
 CC precursors. The present sequence is the hinge, CH2 and CH3 regions of
 CC human IgGgamma1. This sequence can be used to generate fusion proteins of
 CC OPG and immunoglobulin, for use in the present invention. The generated
 CC fusion proteins can exhibit increased circulating half-lives and slower
 CC clearance times, thereby providing a more sustained activity.
 CC
 SQ Sequence 232 AA:
 Query Match 97.2%; Score 1225; DB 22; Length 232;
 Best Local Similarity 97.0%; Pred. No. 2.1e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSDCKHTHTPCPCAPAPLLGSPVFLPPPKKOTLMISRPEVTCVAVDVSHDEPEVKF 60
 DB 1 EPKSDCKHTHTPCPCAPAPLLGSPVFLPPPKKOTLMISRPEVTCVAVDVSHDEPEVKF 60
 QY 61 NMVYDGVVHNKTKPREEOYNSTRVAVSVLTVLHQNMMNGKEYCKYCNKALPAPIEKT 120
 DB 61 NMVYDGVVHNKTKPREEOYNSTRVAVSVLTVLHQNMMNGKEYCKYCNKALPAPIEKT 120
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVWESNGOPENNYKTTTP 180
 DB 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVWESNGOPENNYKTTTP 180
 QY 181 PVLDSGSEFLYSKLTVDKSRWQGNVSCSYMHALNNHYOQRSLSPGK 232
 DB 181 PVLDSGSEFLYSKLTVDKSRWQGNVSCSYMHALNNHYOQRSLSPGK 232
 RESULT 5
 AAE15347
 ID AAE15347 standard; Protein; 232 AA.
 XX
 AC AAE15347;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human immunoglobulin G (IgG) gamma 1 constant heavy chain hinge region.
 XX
 KW Human; erythropoietin; Epo; haematocrit; anaemia; kidney function; IgG;
 KW cancer; myelosuppressive therapy; anti-viral drug; immunoglobulin G.
 XX
 OS Homo sapiens.
 XX
 PN WO200181405-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 19-APR-2001; 2001WO-US12836.
 XX
 PR 21-APR-2000; 2000US-0559001.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Egle JC, Elliott SG, Browne JK, Sitney KC;
 DR WPI: 2002-034433/04.

XX Increasing and maintaining hematocrit in mammal suffering from anemia,
 PT comprising administering hyperglycosylated analog of erythropoietin
 PT less frequently and at lower molar amount of recombinant human
 PT erythropoietin

XX Example 1; Fig 10; 95pp: English.

XX The invention relates to a method for increasing and maintaining
 CC haematocrit in a mammal. The method comprises administering a
 CC hyperglycosylated analogue of erythropoietin (Epo) in a pharmaceutical
 CC composition, less frequently than an equivalent molar amount of and at
 CC a lower molar amount than recombinant human Epo (rhEpo) to obtain a
 CC comparable target haematocrit. Epo is a glycoprotein hormone necessary
 CC for the maturation of erythroid progenitor cells into erythrocytes.
 CC Human Epo analogue is useful for raising and maintaining haematocrit to
 CC a comparable target haematocrit in a mammal suffering from anaemia
 CC associated with a decline or loss of kidney function, myelosuppressive
 CC therapy comprising chemotherapeutic or anti-viral drugs or associated
 CC with excessive blood loss during surgical procedures, and in cancer
 CC condition. The present sequence is human immunoglobulin G (19g) gamma 1
 CC constant heavy chain (CH2, CH3) hinge region used to construct Epo
 CC hyperglycosylated analogue fusion protein.

XX Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 23; Length 232;

Best Local Similarity 97.0%; Pred. No. 2,1e-90;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDTHPCPCPAPPELLGSPVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKF 60
 DB 1 EPKSCDTHPCPCPAPPELLGSPVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKF 60
 QY 61 NMVYDGEVHNVTKPREEOYNSTRVSVLTVLHQMNMNGEKCKVSKALPAPTEKT 120
 DB 61 NMVYDGEVHNVTKPREEOYNSTRVSVLTVLHQMNMNGEKCKVSKALPAPTEKT 120
 QY 121 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AEWESNGQPNNTKTP 180
 DB 121 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AEWESNGQPNNTKTP 180
 QY 121 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AEWESNGQPNNTKTP 180
 DB 121 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AEWESNGQPNNTKTP 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRMOGNGVSCSVHMEALHNHYTKSLSPGK 232
 DB 181 PVLDSVGSFFLYSKLTVDKSRMOGNGVSCSVHMEALHNHYTKSLSPGK 232

RESULT 6

ABB09463 ID ABB09463 standard; Protein: 233 AA.

XX ABB09463;

XX 01-JUL-2002 (first entry)

XX Human IgG Fc fragment amino acid sequence.

XX Protein A; immunoglobulin G; IgG; antibody; human.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT Misc-difference 168

XX FT Misc-difference 169 /note= "encoded by AAC"

XX FT Misc-difference 169 /note= "encoded by AAC"

XX PN WO200204602-A1.

XX PD 17-JAN-2002.

XX PF 04-JUL-2001; 2001WO-JP05788.

PR 07-JUL-2000; 2000JP-0206689.

PA (GENC-) GENCOM CORP.

XX Tanaka A, Ueda M, Teranishi Y;

XX WPI; 2002-148174/19.

XX N-PSDB; ABL52834.

XX Transformant yeast for stable supply of highly active catalytic
 PT antibody, comprises the capability of expressing and presenting protein
 PT A or its fragment, particularly with the 22 domain, on the cell surface

XX Example 3; Fig 4; 25pp: Japanese.

XX The invention relates to a transformant yeast that can present protein A
 CC or its fragment on its cell surface. The yeast can be used for detecting
 CC or isolating the Fc part of immunoglobulin (Ig)G. The yeast is useful for
 CC a stable supply of highly active catalytic antibody e.g. by screening
 CC novel functional molecules and in isolating Fc-carrying secretory
 CC proteins. The yeast of the invention is capable of adhering specifically
 CC to a combinatorial antibody library with an Fc-carrying antibody
 CC component. The current sequence represents the human IgG Fc fragment
 CC amino acid sequence.

XX Sequence 233 AA;

Query Match 97.2%; Score 1225; DB 23; Length 233;

Best Local Similarity 97.0%; Pred. No. 2,1e-90;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDTHPCPCPAPPELLGSPVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKF 60
 DB 2 EPKSCDTHPCPCPAPPELLGSPVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKF 61
 QY 61 NMVYDGEVHNVTKPREEOYNSTRVSVLTVLHQMNMNGEKCKVSKALPAPTEKT 120
 DB 61 NMVYDGEVHNVTKPREEOYNSTRVSVLTVLHQMNMNGEKCKVSKALPAPTEKT 121
 QY 121 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AEWESNGQPNNTKTP 180
 DB 121 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AEWESNGQPNNTKTP 181
 QY 122 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AEWESNGQPNNTKTP 181
 DB 122 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AEWESNGQPNNTKTP 181
 QY 181 PVLDSVGSFFLYSKLTVDKSRMOGNGVSCSVHMEALHNHYTKSLSPGK 232
 DB 182 PVLDSVGSFFLYSKLTVDKSRMOGNGVSCSVHMEALHNHYTKSLSPGK 233

RESULT 7

ABB81490 ID ABB81490 standard; Protein: 251 AA.

XX ABB81490;

XX 02-SEP-2002 (first entry)

XX Human immunoglobulin gamma1 constant region protein SEQ ID NO:18.

XX Human; ZNF12; tumour necrosis factor receptor; cytosolic;

XX immunosuppressive; dermatological; antiinflammatory; antididiabetic;

XX neuroprotective; antirheumatic; antiarthritic; antisthmatic;

XX nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;

XX autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;

XX multiple sclerosis; insulin dependent diabetes mellitus; asthma;

XX rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;

XX glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;

XX pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;

XX light chain neuropathy; hypertension; large vessel disease;

XX graft-versus host disease; graft rejection; Crohn's disease.

XX Homo sapiens.

PN WO200238766-A2.
 XX
 XX 16-MAY-2002.
 XX
 XX 05-NOV-2001; 2001WO-US47018.
 XX
 XX 07-NOV-2000; 2000US-246449P.
 PR 20-DEC-2000; 2000US-257131P.
 PR 28-JUN-2001; 2001US-301715P.
 PR 29-AUG-2001; 2001US-315565P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Gross JA, Xu W, Henne RM, Grant FJ;
 XX
 XX WPI: 2002-508212/54.
 DR N-PSDB: ABN89435.
 XX
 XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end
 PT stage renal failure or renal disease and lymphoma
 XX
 XX Example 4; Page 143; 154pp; English.

XX The present invention describes a human tumour necrosis factor receptor
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. Human Ztnfr12 is located to chromosome 22q13.2. The
 CC present sequence represents human immunoglobulin gamma1 constant region,
 CC which is used in an example from the present invention.

XX Sequence 251 AA;

Query Match 97.2%; Score 1225; DB 23; Length 251;
 Best Local Similarity 97.0%; Pred. No. 2.3e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTPCPPAPAPLLGGPSVFLFPPKPKDTLMISRPPEVTCVAVDVSHEDPEYKF 60
 DB 20 EPKSCDKHTHTPCPPAPAPLLGGPSVFLFPPKPKDTLMISRPPEVTCVAVDVSHEDPEYKF 79
 QY 61 NMVYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDMNKEKCKCKVSNKALPAPIEKT 120
 DB 80 NMVYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDMNKEKCKCKVSNKALPAPIEKT 139
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTTP 180
 DB 140 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTTP 199
 QY 181 PVLDSVGSFFLYSKLTVDKSRMQGQNVFSCSVMEHALHNHYQOQSLSLSPGK 232
 DB 200 PVLDSGGSFFLYSKLTVDKSRMQGQNVFSCSVMEHALHNHYQOQSLSLSPGK 251

RESULT 8
 AAY24154

ID AAY24154 standard; Protein; 259 AA.
 XX
 XX AAY24154;
 AC
 XX
 XX 10-SEP-1999 (first entry)
 DT
 XX
 XX Protein from pc051neg1 comprising human IgG1 Fc region genomic DNA.
 DE
 XX LDL; denatured; oxidised; arteriosclerosis; hyperlipidaemia;
 KW low density lipoprotein; receptor; detection; immunoglobulin;
 KW fusion protein.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX
 XX WO9932520-A1.
 XX
 XX 01-JUL-1999.
 XX
 XX 18-DEC-1998; 98WO-JP05744.
 XX
 XX 16-DEC-1998; 98JP-0358170.
 PR 19-DEC-1997; 97JP-0364981.
 PR 09-DEC-1998; 98JP-0349648.
 XX
 XX (NISB) JAPAN TOBACCO INC.
 PA
 XX
 XX Kakutani M, Masaki T, Sawamura T;
 PI
 XX WPI: 1999-418906/35.
 DR N-PSDB: AAX88533.
 XX
 XX Fusion peptide for assay of oxidized LDL and for therapeutic use

XX Example 1; Page 92-96; 105pp; Japanese.
 PS
 XX The present invention describes a fusion peptide which consists of the
 CC extracellular domain of a mammalian oxidized LDL (low density
 CC lipoprotein) receptor, fused to a partial heavy chain of a mammalian
 CC immunoglobulin containing all or part of the constant region. Oxidized
 CC LDL is a denatured form of LDL occurring in patients having
 CC arteriosclerosis or hyperlipidaemia, and the fusion peptide can be
 CC used for the assay of oxidized LDL in biological samples from such
 CC patients, for the diagnosis of the disorders. It can also be used
 CC therapeutically for the prevention and treatment of arteriosclerosis and
 CC hyperlipidaemia. The present sequence represents the protein from the
 CC vector DNA of pc051neg1 comprising human IgG1 Fc region genomic DNA.

XX Sequence 259 AA;

Query Match 97.2%; Score 1225; DB 20; Length 259;
 Best Local Similarity 97.0%; Pred. No. 2.4e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTPCPPAPAPLLGGPSVFLFPPKPKDTLMISRPPEVTCVAVDVSHEDPEYKF 60
 DB 28 EPKSCDKHTHTPCPPAPAPLLGGPSVFLFPPKPKDTLMISRPPEVTCVAVDVSHEDPEYKF 87
 QY 61 NMVYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDMNKEKCKCKVSNKALPAPIEKT 120
 DB 88 NMVYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDMNKEKCKCKVSNKALPAPIEKT 147
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTTP 180
 DB 148 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTTP 207
 QY 181 PVLDSVGSFFLYSKLTVDKSRMQGQNVFSCSVMEHALHNHYQOQSLSLSPGK 232
 DB 208 PVLDSGGSFFLYSKLTVDKSRMQGQNVFSCSVMEHALHNHYQOQSLSLSPGK 259

RESULT 9
 AAB47590

```

ID AAB47590 standard; Protein: 287 AA.
XX
AC AAB47590;
XX
DT 13-DEC-2001 (first entry)
XX
DE Fusion protein of HSA:human IgG1 Fc.
XX
KW Mouse; heat shock antigen; HSA: human; rat; signal transducer; CD24;
KW fusion protein; inhibition; autoreactive T cell; aTC;
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis;
KW systemic lupus erythematosus; psoriasis; diabetes; allergy;
KW transplant rejection; transgenic mouse.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Mus musculus.
XX
PN W0200172325-A1.
XX
PD 04-OCT-2001.
XX
PF 29-MAR-2001; 2001WO-US40390.
XX
PR 29-MAR-2000; 2000US-192814P.
XX
PA (OHIS ) UNIV OHIO STATE RES FOUND.
XX
PI Liu Y, Zheng P, Bai X;
XX
DR WPI: 2001-611581/70.
DR N-PSDB; AAH43523, AAH43524.
XX
XX
XX Inhibiting tissue destruction by autoreactive T cells, useful for
XX treating autoimmune diseases, by administering a heat-shock
XX antigen/CD24 polypeptide or its antibody
XX
XX Disclosure; Fig 10; 34pp; English.
XX
XX This sequence represents a fusion protein which comprises the mouse
XX heat shock antigen (HSA) fused to human IgG1 Fc. This protein
XX may be used in the method of the invention for inhibiting
XX destruction of tissue initiated by autoreactive T cells (aTC). The
XX method is especially used to treat subjects suspected of having
XX autoimmune diseases, particularly multiple sclerosis, rheumatoid
XX arthritis, systemic lupus erythematosus, psoriasis, diabetes and
XX allergy, also transplant rejection. Transgenic mice that express
XX human CD24 on their T cells are useful as models for testing drugs
XX for use against autoimmune diseases.
XX
XX Sequence 287 AA;
XX
Query Match 97.2%; Score 1225; DB 22; Length 287;
Best Local Similarity 97.0%; Pred. No. 2.8e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
OY 1 EPKSCDTHHCPCPAPPELLGSPVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKF 60
DB 56 EPKSCDTHHCPCPAPPELLGSPVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKF 115
OY 61 NMVYDGEVHNHNAKTKPREQYNSTYRVSVLTVLHQMWMNGKEYCKVSKALPAPIEKT 120
DB 116 NMVYDGEVHNHNAKTKPREQYNSTYRVSVLTVLHQMWMNGKEYCKVSKALPAPIEKT 175
OY 121 ISRAKVGPRPQVYITLPPSRDELTKNOVSLTCLVKGYPSPDIAVEMESNCPENNYKTP 180
DB 176 ISRAKVGPRPQVYITLPPSRDELTKNOVSLTCLVKGYPSPDIAVEMESNCPENNYKTP 235
OY 181 PVLDSVGSFLLYSKLTIVDKSRMOOGNFSVSMHEALHNHYOORSLSLSPGK 232
DB 236 PVLDSVGSFLLYSKLTIVDKSRMOOGNFSVSMHEALHNHYOORSLSLSPGK 287

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AAR91806
ID AAR91806 standard; Protein: 329 AA.
XX
AC AAR91806;
XX
DT 20-SEP-1996 (first entry)
XX
DE Human immunoglobulin gamma heavy chain constant region sequences.
XX
KW alkaline phosphatase; label; antibody; IgG; H-chain; C-region; CH1;
KW CH2; CH3; hinge; fusion protein; chimera; immunoassay.
XX
XX Homo sapiens.
XX
XX JP08070875-A.
XX
PN 19-MAR-1996.
XX
PD 05-SEP-1994; 94JP-0211035.
XX
PF 05-SEP-1994; 94JP-0211035.
XX
PR 05-SEP-1994; 94JP-0211035.
XX
PA (TOYJ ) TOSOH CORP.
XX
XX WPI: 1996-203155/21.
XX
DR N-PSDB; AAT27385.
XX
XX Recombinant alkaline phosphatase (AP)-antibody fusion protein -
XX comprises AP fused downstream of antibody heavy or light chain,
XX useful as immunoassay reagent
XX
XX Example 1; Page 13-15; 44pp; Japanese.
XX
XX The gene coding for human alkaline phosphatase is fused downstream
XX of a gene coding for either the variable and CH1 regions of an
XX antibody heavy chain or an antibody light chain. Coexpression of the
XX H- and L-chain sequences, one of which is fused to the AP gene,
XX results in production of AP-labelled antibodies suitable for use in
XX immunoassays. The present sequence is from a human IgG heavy chain
XX constant region.
XX
XX Sequence 329 AA;
XX
Query Match 97.2%; Score 1225; DB 17; Length 329;
Best Local Similarity 97.0%; Pred. No. 3.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
OY 1 EPKSCDTHHCPCPAPPELLGSPVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKF 60
DB 98 EPKSCDTHHCPCPAPPELLGSPVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKF 157
OY 61 NMVYDGEVHNHNAKTKPREQYNSTYRVSVLTVLHQMWMNGKEYCKVSKALPAPIEKT 120
DB 158 NMVYDGEVHNHNAKTKPREQYNSTYRVSVLTVLHQMWMNGKEYCKVSKALPAPIEKT 217
OY 121 ISRAKVGPRPQVYITLPPSRDELTKNOVSLTCLVKGYPSPDIAVEMESNCPENNYKTP 180
DB 218 ISRAKVGPRPQVYITLPPSRDELTKNOVSLTCLVKGYPSPDIAVEMESNCPENNYKTP 277
OY 181 PVLDSVGSFLLYSKLTIVDKSRMOOGNFSVSMHEALHNHYOORSLSLSPGK 232
DB 278 PVLDSVGSFLLYSKLTIVDKSRMOOGNFSVSMHEALHNHYOORSLSLSPGK 329

```

RESULT 10

```

RESULT 11
ID AAB04071
AAB04071 standard; Protein: 330 AA.
XX
AC AAB04071;
XX
DT 11-APR-2001 (first entry)
XX
DE 2cytor 10::Igg gamma fusion peptide.

```


XX zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;
 KW binding; detection; modulation; recombinant cell;
 KW haematopoietic cell; lymphoid cell; myeloid cell; lymph;
 KW immune system; blood; bone; inflammatory response; inflammation;
 KW spleen; human.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN W0200068381-A1.
 PD 16-NOV-2000.
 PE 11-MAY-2000; 2000WO-US12924.
 PR 11-MAY-1999; 99US-0309861.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 PI Presnell SR, Foster DC, Hammond AK, Lok S;
 DR WPI, 2001-016096/02.
 DR N-PSDB; AAA54473.
 XX
 PT New cytokine receptor mouse zcytor 10, useful for detecting ligands
 PT that stimulate proliferation or development of haematopoietic,
 PT lymphoid and myeloid cells
 XX
 PS Example 17; Page 120-121; 134pp; English.
 XX
 CC Isolating a nucleotide which encodes the zcytor 10 cytokine
 CC receptor enables the production of recombinant cells expressing the
 CC receptor. Those cells can then be used to detect the presence of a
 CC modulator of zcytor10 protein by culturing the cells in the presence
 CC of a test ligand and comparing levels of activity of mouse zcytor10
 CC in the presence and absence of the test sample. Similarly, detection
 CC of zcytor10 receptor ligand within a test sample can be achieved.
 CC The method comprising contacting a test sample containing an amino
 CC acid sequence from Cys15 to Gly25 to Pro230 of the zcytor 10
 CC cytokine receptor and detecting the binding of the polypeptide to a
 CC ligand in the sample. Specified peptide fragments of the zcytor 10
 CC cytokine receptor and the methods described are used to identify
 CC ligands that stimulate the proliferation and/or development of
 CC haematopoietic, lymphoid and myeloid cells. Peptide fragments of
 CC the cytokine receptor are useful for treating lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders and for generating
 CC antibodies directed against the receptor. A vector expressing a
 CC secreted human zcytor 10 heterodimer is constructed. In this
 CC construct the extracellular cytokine binding domain of zcytor 10
 CC is fused to the heavy chain of IgG gamma and the extracellular
 CC portion of the heteromeric cytokine receptor subunit (an
 CC interleukin receptor subunit) is fused to human kappa light
 CC chain (See GENESBQ record AAA54474). The two sequences are fused
 CC together using two primers (AAA54475, AAA54476).
 XX
 SQ Sequence 330 AA;
 Query Match 97.2%; Score 1225; DB 22; Length 330;
 Best local similarity 97.0%; Pred. No. 3.3e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 181 PVLDVSGFFLYSKLFDKSRMOGNYFSCSVMEHLLHNHXRSLSPGK 232
 Db 279 PVLDSDGSFFLYSKLTYDKSRMOGNYFSCSVMEHLLHNHRYTKSLSPGK 330
 RESULT 12
 ID ABB81641 standard; Protein; 330 AA.
 AC ABB81641;
 DT 25-SEP-2002 (first entry)
 DE Human IgG gamma 1 heavy chain SEQ ID NO:15.
 XX
 KW Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic;
 KW antirheumatic; antiarthritic; neuroprotective; antiinflammatory;
 KW antidiabetic; nephrotropic; dermatological; anti-HIV; haemostatic;
 KW vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV;
 KW diabetes mellitus; inflammatory bowel disease; Crohn's disease; asthma;
 KW immunologic renal disease; glomerulonephritis; vasculitis; polyarteritis;
 KW mesangiol proliferative disease; chronic lymphocytic leukaemia; bronchitis;
 KW secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma;
 KW haemolytic uraemic syndrome; renal neoplasm; urological neoplasm;
 KW emphysema; chronic airway disease.
 XX
 OS Homo sapiens.
 PN W0200244209-A2.
 PD 06-JUN-2002.
 PE 28-NOV-2001; 2001WO-US44808.
 PR 28-NOV-2000; 2000US-253561P.
 PR 07-FEB-2001; 2001US-267211P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 PI Presnell SR, Xu W, Novak JE, Whitmore TE, Grant FJ;
 DR WPI, 2002-527700/56.
 DR N-PSDB; ABQ73076.
 XX
 PT Novel zcytor19 polypeptides and polynucleotides useful for stimulating
 PT immune responses in animals for producing antibodies, and for treating
 PT autoimmune diseases, leukemia and asthma
 XX
 PS Example 7; Page 171-172; 200pp; English.
 XX
 CC The present invention describes an isolated human zcytor19 protein (I),
 CC and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic,
 CC antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
 CC antidiabetic, nephrotropic, dermatological, anti-HIV and haemostatic
 CC activities, and can be used in vaccines. (I) or an antibody binding (I)
 CC can be used for suppressing the immune system for reducing rejection of
 CC tissue or organ transplants and grafts and for treating T-cell specific
 CC leukaemias or lymphomas and autoimmune diseases including rheumatoid
 CC arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel
 CC disease and Crohn's disease. The antibodies can also be used for treating
 CC immunologic renal diseases, glomerulonephritis, mesangiol proliferative
 CC disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or
 CC vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related
 CC diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the
 CC antibodies can also be used for renal or urological neoplasms and
 CC multiple myelomas, asthma, bronchitis, emphysema and other chronic
 CC airway diseases. Human zcytor19 is located to chromosome 1, more
 CC specifically to chromosome 1p36.11. The present sequence represents
 CC a human IgG gamma 1 heavy chain protein, which is used in an example
 CC from the present invention.
 XX

Sequence 330 AA;
 Query Match 97.2%; Score 1225; DB 23; Length 330;
 Best Local Similarity 97.0%; Pred. No. 3.3e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHHCPCPPAPPELLGSPVFLFPKPKDTLMISRTPEVTCVAVVDSHEDPEVKF 60
 |||||
 DB 99 EPKSCDKTHHCPCPPAPPELLGSPVFLFPKPKDTLMISRTPEVTCVAVVDSHEDPEVKF 158
 QY 61 NWYDGVGVHNAKTRPREEOYNSTYRVVSVLTVLHOMMNGKEKCKVSKALPAPLEKT 120
 |||||
 DB 159 NWYDGVGVHNAKTRPREEOYNSTYRVVSVLTVLHOMMNGKEKCKVSKALPAPLEKT 218
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTP 180
 |||||
 DB 219 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTP 278
 QY 181 PVLDVSGSFLLYSKLTVDKSRMOOGNVSFSCVMHEALHNHYQKSLSPGK 232
 |||||
 DB 279 PVLDVSGSFLLYSKLTVDKSRMOOGNVSFSCVMHEALHNHYQKSLSPGK 330

RESULT 13
 ID AAE21960; standard; Protein: 330 AA.
 AC AAE21960;
 DT 25-JUL-2002 (first entry)
 XX
 DE Human death domain containing receptor (DR6). protein-related protein.
 XX
 KW Human; therapy; death domain containing receptor; DR6; receptor; anaemia;
 KW apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;
 KW diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis;
 KW transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis;
 KW autoimmune gastritis; dermatosis; cardiopathy; infertility; haemostatic;
 KW H. pylori-associated ulceration; anti-inflammatory; vasotropic; vitreous;
 KW acquired immunodeficiency syndrome; AIDS; human immunodeficiency virus;
 KW HIV; haemolytic uremic syndrome; HUS; immunodeficiency; neuroprotective;
 KW adult respiratory distress syndrome; ARDS; cytosolic; thymimetic;
 KW dematological; hepatotropic; antibacterial.
 KW
 XX Homo sapiens.
 OS
 XX
 PN WO200185209-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 30-APR-2001; 2001WO-US11735.
 XX
 PR 10-MAY-2000; 2000US-203015P.
 XX
 PA (ELIL) LILLY & CO ELI.
 PI Heuer JG, Liu J, Na S, Song HY, Yang D;
 DR WPI; 2002-351283/38.
 XX
 PT Treating or preventing T cell or Th2 cell mediated condition e.g.,
 PT asthma or multiple sclerosis in mammal, comprises administering
 PT composition comprising death domain containing receptor, DR6 agonist or
 PT antagonist.
 XX
 PS Disclosure; Page 132-133; 133pp; English.
 XX
 CC The invention relates to a method for treating or preventing a T cell
 CC mediated condition or a Th2 cell mediated condition in a mammal. The
 CC method comprising administering to the mammal a pharmaceutical
 CC composition comprising a death domain containing receptor (DR6) agonist
 CC or antagonist. The method is useful for treating or preventing a T cell
 CC mediated condition or a Th2 cell mediated condition in a mammal. A DR6

CC agonist is useful in the manufacture of a medicament for treating or
 CC preventing at least one symptom associated with aberrant apoptosis,
 CC graft-versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma,
 CC atopy, inflammatory bowel disease, vasculitis, psoriasis, pancreatitis,
 CC insulin-dependent diabetes mellitus, cancer, multiple sclerosis,
 CC Hashimoto's thyroiditis, Graves disease, transplant rejection, systemic
 CC lupus erythematosus, autoimmune dermatosis, autoimmune cardiopathy,
 CC autoimmune infertility, Behcet's disease, autoimmune gastritis, fibrosing
 CC lung disease, organ rejection after transplantation, thrombotic
 CC thrombocytopenic purpura (TTP), chronic glomerulonephritis, haemolytic
 CC uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ
 CC dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS)
 CC or a condition or symptom related to the above mentioned diseases in a
 CC mammal. An DR6 antagonist is useful in the manufacture of a medicament
 CC for treating or preventing at least one symptom associated with
 CC immunodeficiency, aberrant apoptosis, bacterial, viral or microbial
 CC infection, complications of infection, human immunodeficiency virus
 CC (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency
 CC syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis
 CC C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori
 CC associated ulceration, cytoprotection during cancer treatment,
 CC recuperation from chemotherapy, recuperation from irradiation therapy,
 CC or a condition or symptom related to the above mentioned diseases in a
 CC mammal. The present sequence is human DR6 protein-related protein.
 CC
 XX

Sequence 330 AA;
 Query Match 97.2%; Score 1225; DB 23; Length 330;
 Best Local Similarity 97.0%; Pred. No. 3.3e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHHCPCPPAPPELLGSPVFLFPKPKDTLMISRTPEVTCVAVVDSHEDPEVKF 60
 |||||
 DB 99 EPKSCDKTHHCPCPPAPPELLGSPVFLFPKPKDTLMISRTPEVTCVAVVDSHEDPEVKF 158
 QY 61 NWYDGVGVHNAKTRPREEOYNSTYRVVSVLTVLHOMMNGKEKCKVSKALPAPLEKT 120
 |||||
 DB 159 NWYDGVGVHNAKTRPREEOYNSTYRVVSVLTVLHOMMNGKEKCKVSKALPAPLEKT 218
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTP 180
 |||||
 DB 219 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTP 278
 QY 181 PVLDVSGSFLLYSKLTVDKSRMOOGNVSFSCVMHEALHNHYQKSLSPGK 232
 |||||
 DB 279 PVLDVSGSFLLYSKLTVDKSRMOOGNVSFSCVMHEALHNHYQKSLSPGK 330

RESULT 14
 ID ABB05736
 AC ABB05736; standard; Protein: 330 AA.
 DT 01-MAY-2002 (first entry)
 XX
 DE Human immunoglobulin G gamma 1 protein sequence SEQ ID NO:38.
 XX
 KW Zeytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
 KW anti-inflammatory; antiviral; antirheumatic; antiarthritic; cytoskeletal;
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
 KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW inflammatory disease; pancreatitis; inflammatory bowel disease.
 KW
 XX Homo sapiens.
 OS
 XX
 PN WO200200721-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 26-JUN-2001; 2001WO-US20484.
 XX

PR 26-JUN-2000; 2000US-214282P.
 PR 29-JUN-2000; 2000US-214955P.
 PR 08-FEB-2001; 2001US-267963P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuljper JL;
 PI Maurer MF;
 XX
 DR WPI: 2002-090519/12.
 DR N-PSDB; ABA93797.
 XX
 PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders -
 XX
 PS Example 17; Page 187-188; 235pp; English.
 XX
 CC The present invention describes a cytokine receptor designated zcytor17.
 CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
 CC antirheumatic, antiarthritic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or
 CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
 CC immunity and for stimulating lymphocyte proliferation, such as in the
 CC treatment of infections involving immunosuppression, including certain
 CC viral infections. They are also useful for inducing cytotoxicity and
 CC for treating leukemias. Antagonist of zcytor17 polypeptides are useful
 CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 330 AA:
 QO
 Query Match 97.2%; Score 1225; DB 23; Length 330;
 Best Local Similarity 97.0%; Pred. No. 3.3e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDTHTCPPCPAPPELLGSPVFLFPPPKRPTLMISRPEYTCVVDVSHDPEYKF 60
 DB 99 EPKSCDTHTCPPCPAPPELLGSPVFLFPPPKRPTLMISRPEYTCVVDVSHDPEYKF 158
 QY 61 NMVYDGEVHNKTKPREEOYNSTYRVSVLTVLHOMMNGKEKCKVSNKALPAPIEKT 120
 DB 159 NMVYDGEVHNKTKPREEOYNSTYRVSVLTVLHOMMNGKEKCKVSNKALPAPIEKT 218
 QY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEWESNGPENNYKTP 180
 DB 219 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEWESNGPENNYKTP 278
 QY 181 PVLDSVGSFLLYSKLTVDKSRMOGNNFSCSVMEHALHNHQORSLSLSPGK 232
 DB 279 PVLDSGDSFLLYSKLTVDKSRMOGNNFSCSVMEHALHNHYTKSLSLSPGK 330
 RESULT 15
 ID AAM47856 standard; Protein; 330 AA.
 AC AAM47856;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 XX Human Ig-gamma1 heavy chain constant region amino acid sequence.
 DE
 XX Human Ig-gamma1 heavy chain constant region amino acid sequence.
 XX
 KW Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;
 KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
 transgenic plant.
 XX
 OS Homo sapiens.

XX
 PN WO200183529-A2.
 XX
 PD 08-NOV-2001.
 XX
 PE 28-APR-2001; 2001WO-US13932.
 XX
 PR 28-APR-2000; 2000US-200298P.
 XX
 PA (PLAN-) PLANET BIOTECHNOLOGY INC.
 XX
 PI Larrick JW, Wycoff KL;
 PI WPI: 2002-041481/05.
 DR N-PSDB; ABA05265.
 XX
 PT Immunoadhesin for treating human rhinovirus infection comprises
 PT chimeric intercellular adhesion molecule-1, and optionally a J chain
 PT and secretory component in association -
 XX
 PS Disclosure; Fig 7; 138pp; English.
 XX
 CC The invention relates to an immunoadhesin comprising:
 CC (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a
 CC rhinovirus receptor protein linked to at least a portion of an
 CC immunoglobulin heavy chain; and
 CC (b) optionally a J chain and secretory component associated with the
 CC chimeric ICAM-1 molecule. The immunoadhesin has plant-specific
 CC glycosylation and virucide activity. The immunoadhesin is useful for
 CC reducing infection by human rhinovirus (HRV) and hence the initiation or
 CC spread of the common cold by HRV. The immunoadhesin binds to HRV and
 CC reduces its infectivity, competing with cell surface ICAM-1 for binding
 CC sites, interfering with virus entry or uncoating and directing premature
 CC release of viral RNA and formation of empty capsids. Expression of the
 CC immunoadhesin in plants would be tetrameric, rather than dimeric.
 CC Immunoadhesin having multiple binding sites have a higher effective
 CC affinity for the virus, thereby increasing the effectiveness of the
 CC immunoadhesin. Association of secretory component and immunoglobulin J
 CC chain increases the stability of the immunoadhesin in the mucosal
 CC environment. Production is significantly less expensive in plants than in
 CC animal cell culture and production in plants is safer for human use,
 CC since plants are not known to harbor any animal viruses. The present
 CC sequence is that of a human immunoglobulin protein sequence, useful to
 CC the invention.
 XX
 XX Sequence 330 AA:
 QO
 Query Match 97.2%; Score 1225; DB 23; Length 330;
 Best Local Similarity 97.0%; Pred. No. 3.3e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDTHTCPPCPAPPELLGSPVFLFPPPKRPTLMISRPEYTCVVDVSHDPEYKF 60
 DB 99 EPKSCDTHTCPPCPAPPELLGSPVFLFPPPKRPTLMISRPEYTCVVDVSHDPEYKF 158
 QY 61 NMVYDGEVHNKTKPREEOYNSTYRVSVLTVLHOMMNGKEKCKVSNKALPAPIEKT 120
 DB 159 NMVYDGEVHNKTKPREEOYNSTYRVSVLTVLHOMMNGKEKCKVSNKALPAPIEKT 218
 QY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEWESNGPENNYKTP 180
 DB 219 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEWESNGPENNYKTP 278
 QY 181 PVLDSVGSFLLYSKLTVDKSRMOGNNFSCSVMEHALHNHQORSLSLSPGK 232
 DB 279 PVLDSGDSFLLYSKLTVDKSRMOGNNFSCSVMEHALHNHYTKSLSLSPGK 330

Search completed: July 15, 2003, 06:57:38
 Job time : 29.3185 secs

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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:59:40 ; Search time 17.7984 Seconds

(without alignments)
1517.518 Million cell updates/sec

Title: US-09-847-208B-3

Perfect score: 1260

Sequence: 1 EPKSCDKHTPCPCAPPELL.....MHEALHNHYQORSLSPGK 232

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PC7_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/PC7IS_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------------|---------------------|
| 1 | 1260 | 100.0 | 232 | US-09-847-208-3 | Sequence 3, Appl1 |
| 2 | 1260 | 100.0 | 330 | US-09-847-208-2 | Sequence 2, Appl1 |
| 3 | 1260 | 100.0 | 569 | US-09-847-208-7 | Sequence 7, Appl1 |
| 4 | 1225 | 97.2 | 232 | US-09-996-357-10 | Sequence 10, Appl1 |
| 5 | 1225 | 97.2 | 235 | US-10-207-655-208 | Sequence 208, Appl1 |
| 6 | 1225 | 97.2 | 247 | US-09-996-357-13 | Sequence 13, Appl1 |
| 7 | 1225 | 97.2 | 251 | US-10-008-063-18 | Sequence 18, Appl1 |
| 8 | 1225 | 97.2 | 251 | US-10-152-363A-6 | Sequence 6, Appl1 |
| 9 | 1225 | 97.2 | 267 | US-09-996-357-12 | Sequence 12, Appl1 |
| 10 | 1225 | 97.2 | 288 | US-09-822-851B-14 | Sequence 14, Appl1 |
| 11 | 1225 | 97.2 | 288 | US-10-119-637A-14 | Sequence 14, Appl1 |
| 12 | 1225 | 97.2 | 330 | US-10-047-542-20 | Sequence 20, Appl1 |
| 13 | 1225 | 97.2 | 330 | US-09-995-896A-15 | Sequence 15, Appl1 |
| 14 | 1225 | 97.2 | 330 | US-09-892-949-38 | Sequence 38, Appl1 |
| 15 | 1225 | 97.2 | 330 | US-10-269-805-68 | Sequence 68, Appl1 |
| 16 | 1225 | 97.2 | 331 | US-10-341-836-2 | Sequence 2, Appl1 |
| 17 | 1225 | 97.2 | 332 | US-09-990-586-98 | Sequence 98, Appl1 |
| 18 | 1225 | 97.2 | 358 | US-10-233-150-5 | Sequence 5, Appl1 |
| 19 | 1225 | 97.2 | 360 | US-09-949-713-11 | Sequence 11, Appl1 |

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| 20 | 1225 | 97.2 | 376 | US-10-084-139-10 | Sequence 10, Appl1 |
| 21 | 1225 | 97.2 | 376 | US-09-949-713-22 | Sequence 22, Appl1 |
| 22 | 1225 | 97.2 | 396 | US-10-193-616-14 | Sequence 14, Appl1 |
| 23 | 1225 | 97.2 | 404 | US-09-948-018-16 | Sequence 16, Appl1 |
| 24 | 1225 | 97.2 | 444 | US-10-150-475A-6 | Sequence 6, Appl1 |
| 25 | 1225 | 97.2 | 447 | US-09-256-156-1 | Sequence 1, Appl1 |
| 26 | 1225 | 97.2 | 451 | US-10-077-023-17 | Sequence 17, Appl1 |
| 27 | 1225 | 97.2 | 451 | US-09-875-338-17 | Sequence 17, Appl1 |
| 28 | 1225 | 97.2 | 451 | US-09-822-698A-26 | Sequence 26, Appl1 |
| 29 | 1225 | 97.2 | 475 | US-09-740-002-27 | Sequence 27, Appl1 |
| 30 | 1225 | 97.2 | 476 | US-10-124-905-4 | Sequence 4, Appl1 |
| 31 | 1225 | 97.2 | 476 | US-10-124-905-12 | Sequence 12, Appl1 |
| 32 | 1225 | 97.2 | 476 | US-09-948-429B-4 | Sequence 4, Appl1 |
| 33 | 1225 | 97.2 | 476 | US-09-948-429B-12 | Sequence 12, Appl1 |
| 34 | 1225 | 97.2 | 476 | US-10-290-703-3 | Sequence 3, Appl1 |
| 35 | 1225 | 97.2 | 476 | US-09-747-669-3 | Sequence 3, Appl1 |
| 36 | 1225 | 97.2 | 478 | US-10-124-905-8 | Sequence 8, Appl1 |
| 37 | 1225 | 97.2 | 478 | US-09-948-429B-8 | Sequence 8, Appl1 |
| 38 | 1225 | 97.2 | 480 | US-10-077-023-5 | Sequence 5, Appl1 |
| 39 | 1225 | 97.2 | 480 | US-10-077-023-133 | Sequence 133, Appl1 |
| 40 | 1225 | 97.2 | 480 | US-10-077-023-135 | Sequence 135, Appl1 |
| 41 | 1225 | 97.2 | 480 | US-09-875-338-5 | Sequence 5, Appl1 |
| 42 | 1225 | 97.2 | 492 | US-10-207-655-344 | Sequence 344, Appl1 |
| 43 | 1225 | 97.2 | 499 | US-10-207-655-15 | Sequence 15, Appl1 |
| 44 | 1225 | 97.2 | 499 | US-10-207-655-148 | Sequence 148, Appl1 |
| 45 | 1225 | 97.2 | 500 | US-10-207-655-240 | Sequence 240, Appl1 |

ALIGNMENTS

RESULT 1
US-09-847-208-3
; Sequence 3, Application US/09847208
; Publication No. US20030082190A1

GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daoceng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-3

Query Match 100.0%; Score 1260; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.6e-88;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | EPKSCDKHTPCPCAPPELLGGPSVFLFPPPKKDTLMTSRPEVTCVVVDVSHEDPEYKF | 60 |
| DB | 1 | EPKSCDKHTPCPCAPPELLGGPSVFLFPPPKKDTLMTSRPEVTCVVVDVSHEDPEYKF | 60 |
| QY | 61 | NNYVDGVEYHNKTRPREQYNSYTRYVSVLTFLHQNMMNGKEYCKVSNKALPAPIEKT | 120 |
| DB | 61 | NNYVDGVEYHNKTRPREQYNSYTRYVSVLTFLHQNMMNGKEYCKVSNKALPAPIEKT | 120 |
| QY | 121 | ISKAVQPREPOVYTLPPSRDELTKNQVSLTLYVGIFYSDI LAVENESNGQENNYKTP | 180 |
| DB | 121 | ISKAVQPREPOVYTLPPSRDELTKNQVSLTLYVGIFYSDI LAVENESNGQENNYKTP | 180 |
| QY | 181 | PVLDVSGSFYLSKLTVDKSRMQGQVNFSCSYMHALHNHYQORSLSPGK 232 | |
| DB | 181 | PVLDVSGSFYLSKLTVDKSRMQGQVNFSCSYMHALHNHYQORSLSPGK 232 | |

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RESULT 2
US-09-847-208-2
; Sequence 2, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; FILE REFERENCE: U667.002A
; CURRENT APPLICATION NUMBER: US/09/847.208
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-2

Query Match
Best Local Similarity 100.0%; Score 1260; DB 9; Length 330;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EPKSCDTHTCPCPAPABELLGSPVFLPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
DB 99 EPKSCDTHTCPCPAPABELLGSPVFLPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 158
OY 61 NMVYDGEVHNKTKPREQYNSTYRVYSLTVLHOMNMNGEKCKVSNKALPAPIEKT 120
DB 159 NMVYDGEVHNKTKPREQYNSTYRVYSLTVLHOMNMNGEKCKVSNKALPAPIEKT 218
OY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGOPENNYKTP 180
DB 219 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGOPENNYKTP 278
OY 181 PVLDVSGSFLLYSLKLTVDKSRMOGQNFSCVMHEALHNHYOQNSLSLSGPK 232
DB 279 PVLDVSGSFLLYSLKLTVDKSRMOGQNFSCVMHEALHNHYOQNSLSLSGPK 330

RESULT 3
US-09-847-208-7
; Sequence 7, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; FILE REFERENCE: U667.002A
; CURRENT APPLICATION NUMBER: US/09/847.208
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (19G1) to CH2-CH3-CH4
; OTHER INFORMATION: (19G)
US-09-847-208-7

Query Match
Best Local Similarity 100.0%; Score 1260; DB 9; Length 569;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EPKSCDTHTCPCPAPABELLGSPVFLPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
DB 1 EPKSCDTHTCPCPAPABELLGSPVFLPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
OY 1 EPKSCDTHTCPCPAPABELLGSPVFLPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
DB 1 EPKSCDTHTCPCPAPABELLGSPVFLPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
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```
RESULT 4
US-09-996-357-10
; Sequence 10, Application US/09996357
; Patent No. US20020133001A1
; GENERAL INFORMATION:
; APPLICANT: Gelfer, Malcolm L
; APPLICANT: Isreal, David I
; APPLICANT: Joyal, John L
; APPLICANT: Gosselin, Michael
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
; FILE REFERENCE: PPI-105
; CURRENT APPLICATION NUMBER: US/09/996.357
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/253,302
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/250,198
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/257,186
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 10
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-357-10

Query Match
Best Local Similarity 97.2%; Score 1225; DB 10; Length 232;
Matches 223; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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DB 1 EPKSCDTHTCPCPAPABELLGSPVFLPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
OY 61 NMVYDGEVHNKTKPREQYNSTYRVYSLTVLHOMNMNGEKCKVSNKALPAPIEKT 120
DB 61 NMVYDGEVHNKTKPREQYNSTYRVYSLTVLHOMNMNGEKCKVSNKALPAPIEKT 120
OY 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGOPENNYKTP 180
DB 121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGOPENNYKTP 180
OY 181 PVLDVSGSFLLYSLKLTVDKSRMOGQNFSCVMHEALHNHYOQNSLSLSGPK 232
DB 181 PVLDVSGSFLLYSLKLTVDKSRMOGQNFSCVMHEALHNHYOQNSLSLSGPK 232

RESULT 5
US-10-207-655-208
; Sequence 208, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207.655
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;; CURRENT FILING DATE: 2002-07-25
;; NUMBER OF SEQ ID NOS: 426
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 208
;; LENGTH: 235
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Fusion polypeptide
US-10-207-655-208

Query Match 97.2%; Score 1225; DB 9; Length 235;
Best Local Similarity 97.0%; Pred. No. 7.6e-86;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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QY 61 NMVYDGVGVHNVKTKPREQYNSTYRVVSVLTVLHQDNMNGEKYCKYKNKALPAPIEKT 120
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QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYGYPSDIAVEMESNGQPENNYKTPP 180
DB 124 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYGYPSDIAVEMESNGQPENNYKTPP 183
QY 181 PVLDSVGSFFLYSKLTVDKSRMVGQGVFNFCGVMHDLNHNHYQOQSLSLSPGK 232
DB 184 PVLDSGGSFFLYSKLTVDKSRMVGQGVFNFCGVMHDLNHNHYQOQSLSLSPGK 235

RESULT 6

US-09-996-357-13
;; Sequence 13, Application US/09996357
;; Patent No. US20020133001A1
;; GENERAL INFORMATION:
;; APPLICANT: Geffer, Malcolm L
;; APPLICANT: Isreal, David I
;; APPLICANT: Joyal, John L
;; APPLICANT: Gosselin, Michael
;; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
;; TITLE OF INVENTION: TREATING AN AMYLOIDOTIC DISEASE
;; FILE REFERENCE: PPI-105
;; CURRENT APPLICATION NUMBER: US/09/996,357
;; PRIOR FILING DATE: 2001-11-27
;; PRIOR APPLICATION NUMBER: 60/253,302
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/250,198
;; PRIOR FILING DATE: 2000-11-29
;; PRIOR APPLICATION NUMBER: 60/257,186
;; PRIOR FILING DATE: 2000-12-20
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 13
;; LENGTH: 247
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-996-357-13

Query Match 97.2%; Score 1225; DB 10; Length 247;
Best Local Similarity 97.0%; Pred. No. 8e-86;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 16 EPKSCDKHTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 75
QY 61 NMVYDGVGVHNVKTKPREQYNSTYRVVSVLTVLHQDNMNGEKYCKYKNKALPAPIEKT 120
DB 76 NMVYDGVGVHNVKTKPREQYNSTYRVVSVLTVLHQDNLNGEKYCKYKNKALPAPIEKT 135
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYGYPSDIAVEMESNGQPENNYKTPP 180

DB 136 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYGYPSDIAVEMESNGQPENNYKTPP 195
QY 181 PVLDSVGSFFLYSKLTVDKSRMVGQGVFNFCGVMHDLNHNHYQOQSLSLSPGK 232
DB 196 PVLDSGGSFFLYSKLTVDKSRMVGQGVFNFCGVMHDLNHNHYQOQSLSLSPGK 247

RESULT 7

US-10-008-063-18
;; Sequence 18, Application US/10008063
;; Publication No. US20030092164A1
;; GENERAL INFORMATION:
;; APPLICANT: Xu, Wenfeng
;; APPLICANT: Henne, Randal M.
;; APPLICANT: Grant, Francis J.
;; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
;; FILE REFERENCE: 00-103
;; CURRENT APPLICATION NUMBER: US/10/008,063
;; CURRENT FILING DATE: 2001-11-05
;; NUMBER OF SEQ ID NOS: 46
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 18
;; LENGTH: 251
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-008-063-18

Query Match 97.2%; Score 1225; DB 9; Length 251;
Best Local Similarity 97.0%; Pred. No. 8.2e-86;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 20 EPKSCDKHTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 79
QY 61 NMVYDGVGVHNVKTKPREQYNSTYRVVSVLTVLHQDNMNGEKYCKYKNKALPAPIEKT 120
DB 80 NMVYDGVGVHNVKTKPREQYNSTYRVVSVLTVLHQDNLNGEKYCKYKNKALPAPIEKT 139
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYGYPSDIAVEMESNGQPENNYKTPP 180
DB 140 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYGYPSDIAVEMESNGQPENNYKTPP 199
QY 181 PVLDSVGSFFLYSKLTVDKSRMVGQGVFNFCGVMHDLNHNHYQOQSLSLSPGK 232
DB 200 PVLDSGGSFFLYSKLTVDKSRMVGQGVFNFCGVMHDLNHNHYQOQSLSLSPGK 251

RESULT 8

US-10-152-363A-6
;; Sequence 6, Application US/10152363A
;; Publication No. US20030103986A1
;; GENERAL INFORMATION:
;; APPLICANT: Rixon, Mark W.
;; APPLICANT: Gross, Jane A.
;; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
;; FILE REFERENCE: 01-20
;; CURRENT APPLICATION NUMBER: US/10/152,363A
;; CURRENT FILING DATE: 2002-05-20
;; PRIOR APPLICATION NUMBER: 60/293,343
;; PRIOR FILING DATE: 2001-05-24
;; NUMBER OF SEQ ID NOS: 70
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 6
;; LENGTH: 251
;; TYPE: PRT
;; ORGANISM: Homo Sapiens
US-10-152-363A-6

Query Match 97.2%; Score 1225; DB 9; Length 251;
Best Local Similarity 97.0%; Pred. No. 8.2e-86;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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OY 1 EPKSCDKTHHTCPPCAPAPELLGSPVFLPPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
    |||
Db 20 EPKSCDKTHHTCPPCAPAPELLGSPVFLPPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 79
    |||
OY 61 NMVYDGEVHNHAKTKPREEOYNSTYRVSVTLVHOMNMCKEYCKVSNKALPAPIEKT 120
    |||
Db 80 NMVYDGEVHNHAKTKPREEOYNSTYRVSVTLVHOMNMCKEYCKVSNKALPAPIEKT 139
    |||
OY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEMESNGOPENNKTTP 180
    |||
Db 140 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEMESNGOPENNKTTP 199
    |||
OY 181 PVLDSGSEFLYSKLTVDKSRMOQGNVSCSVMHGALHNHYQOQSLSPGK 232
    |||
Db 200 PVLDSGSEFLYSKLTVDKSRMOQGNVSCSVMHGALHNHYQOQSLSPGK 251
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RESULT 9
US-09-996-357-12

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; Sequence 12, Application US/0996357
; Patent No. US20020133001A1
; GENERAL INFORMATION:
; APPLICANT: Gefter, Malcolm L
; APPLICANT: Isreal, David I
; APPLICANT: Joyal, John L
; APPLICANT: Gosselin, Michael
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
; FILE REFERENCE: PPI-105
; CURRENT APPLICATION NUMBER: US/09/996,357
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/253,302
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/250,198
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/257,186
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:alpha-beta(16-30)Fc
US-09-996-357-12
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Query Match 97.2%; Score 1225; DB 10; Length 267;

Best Local Similarity 97.0%; Pred. No. 8.8e-86;

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Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
OY 1 EPKSCDKTHHTCPPCAPAPELLGSPVFLPPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
    |||
Db 36 EPKSCDKTHHTCPPCAPAPELLGSPVFLPPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 95
    |||
OY 61 NMVYDGEVHNHAKTKPREEOYNSTYRVSVTLVHOMNMCKEYCKVSNKALPAPIEKT 120
    |||
Db 96 NMVYDGEVHNHAKTKPREEOYNSTYRVSVTLVHOMNMCKEYCKVSNKALPAPIEKT 155
    |||
OY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEMESNGOPENNKTTP 180
    |||
Db 156 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEMESNGOPENNKTTP 215
    |||
OY 181 PVLDSGSEFLYSKLTVDKSRMOQGNVSCSVMHGALHNHYQOQSLSPGK 232
    |||
Db 216 PVLDSGSEFLYSKLTVDKSRMOQGNVSCSVMHGALHNHYQOQSLSPGK 267
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RESULT 10
US-09-822-851B-14
; Sequence 14, Application US/09822851B

Publication No. US20030095966A1

```
; GENERAL INFORMATION:
; APPLICANT: Liu, Yang
; APPLICANT: Zheng, Pan
; APPLICANT: Bai, Xue-Feng
; TITLE OF INVENTION: Methods of Blocking Tissue Destruction by Autoreactive T Cells
; FILE REFERENCE: 22727/04047
; CURRENT APPLICATION NUMBER: US/09/822,851B
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: residues 1-52 are mouse HSA sequences, residues 53-55 are unk
; OTHER INFORMATION: sequences, residues 56-288 are human IgG1 Fc sequences
US-09-822-851B-14
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Query Match 97.2%; Score 1225; DB 9; Length 288;

Best Local Similarity 97.0%; Pred. No. 9.6e-86;

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Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
OY 1 EPKSCDKTHHTCPPCAPAPELLGSPVFLPPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
    |||
Db 56 EPKSCDKTHHTCPPCAPAPELLGSPVFLPPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 115
    |||
OY 61 NMVYDGEVHNHAKTKPREEOYNSTYRVSVTLVHOMNMCKEYCKVSNKALPAPIEKT 120
    |||
Db 116 NMVYDGEVHNHAKTKPREEOYNSTYRVSVTLVHOMNMCKEYCKVSNKALPAPIEKT 175
    |||
OY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEMESNGOPENNKTTP 180
    |||
Db 176 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEMESNGOPENNKTTP 235
    |||
OY 181 PVLDSGSEFLYSKLTVDKSRMOQGNVSCSVMHGALHNHYQOQSLSPGK 232
    |||
Db 236 PVLDSGSEFLYSKLTVDKSRMOQGNVSCSVMHGALHNHYQOQSLSPGK 287
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RESULT 11
US-10-119-637A-14

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; Sequence 14, Application US/10119637A
; Publication No. US20030106084A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Yang
; APPLICANT: Bai, Xue-Feng
; APPLICANT: Zheng, Pan
; TITLE OF INVENTION: Methods of Blocking Tissue Destruction by Autoreactive T Cells
; FILE REFERENCE: 22727/04117
; CURRENT APPLICATION NUMBER: US/10/119,637A
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/822,851
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/192,814
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(52)
; OTHER INFORMATION: mouse HSA
; NAME/KEY: DOMAIN
; LOCATION: (53)..(55)
; OTHER INFORMATION: sequence created by inventor; not from any known organism
; FEATURE:
```


NAME/KEY: DOMAIN
LOCATION: (56)..(288)
OTHER INFORMATION: human Ig1 Fc
US-10-119-637A-14

Query Match 97.2%; Score 1225; DB 9; Length 288;
Best Local Similarity 97.0%; Pred. No. 9.6e-86;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDTHTCPCPAPPELLGGPSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 60
DB 56 EPKSCDTHTCPCPAPPELLGGPSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 115
QY 61 NMVYDGVENHNAKTKPREQYNSTYRVVSVLTVTHQNMNMKEVKCYSNKAALPAPIEKT 120
DB 116 NMVYDGVENHNAKTKPREQYNSTYRVVSVLTVTHQNMNMKEVKCYSNKAALPAPIEKT 175
QY 121 ISKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTTP 180
DB 176 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTTP 235
QY 181 PVLDSVGSFPLYSKLTVDKSRMOQGNVFSQSVMEHALHNHYTQKSLSPGK 232
DB 236 PVLDSGGSFPLYSKLTVDKSRMOQGNVFSQSVMEHALHNHYTQKSLSPGK 287

RESULT 12

US-10-047-542-20
Sequence 20, Application US/10047542
Patent No. US20020168367A1

GENERAL INFORMATION:
APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.C1P1
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
US-10-047-542-20

Query Match 97.2%; Score 1225; DB 9; Length 330;
Best Local Similarity 97.0%; Pred. No. 1.1e-85;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDTHTCPCPAPPELLGGPSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKSCDTHTCPCPAPPELLGGPSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 158
QY 61 NMVYDGVENHNAKTKPREQYNSTYRVVSVLTVTHQNMNMKEVKCYSNKAALPAPIEKT 120
DB 159 NMVYDGVENHNAKTKPREQYNSTYRVVSVLTVTHQNMNMKEVKCYSNKAALPAPIEKT 218
QY 121 ISKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTTP 180
DB 219 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTTP 278
QY 181 PVLDSVGSFPLYSKLTVDKSRMOQGNVFSQSVMEHALHNHYTQKSLSPGK 232
DB 279 PVLDSGGSFPLYSKLTVDKSRMOQGNVFSQSVMEHALHNHYTQKSLSPGK 330

RESULT 13

US-09-995-898A-15

Sequence 15, Application US/09995898A
Publication No. US20030027253A1

GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Xu, Wenteng
APPLICANT: No. US20030027253A1ak, Julia E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Grant, Francis J.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
FILE REFERENCE: 00-108
CURRENT APPLICATION NUMBER: US/09/995,898A
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/253,561
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/267,211
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
US-09-995-898A-15

Query Match 97.2%; Score 1225; DB 9; Length 330;
Best Local Similarity 97.0%; Pred. No. 1.1e-85;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDTHTCPCPAPPELLGGPSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKSCDTHTCPCPAPPELLGGPSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 158
QY 61 NMVYDGVENHNAKTKPREQYNSTYRVVSVLTVTHQNMNMKEVKCYSNKAALPAPIEKT 120
DB 159 NMVYDGVENHNAKTKPREQYNSTYRVVSVLTVTHQNMNMKEVKCYSNKAALPAPIEKT 218
QY 121 ISKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTTP 180
DB 219 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTTP 278
QY 181 PVLDSVGSFPLYSKLTVDKSRMOQGNVFSQSVMEHALHNHYTQKSLSPGK 232
DB 279 PVLDSGGSFPLYSKLTVDKSRMOQGNVFSQSVMEHALHNHYTQKSLSPGK 330

RESULT 14

US-09-892-949-38
Sequence 38, Application US/09892949
Publication No. US20030096339A1

GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.
APPLICANT: Kullper, Joseph L.
APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 38
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
US-09-892-949-38

Query Match 97.2%; Score:1225; DB 9; Length 330;
Best Local Similarity 97.0%; Pred. No.1.le-85;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKRDTLMISRPEVTQVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKRDTLMISRPEVTQVVDVSHEDPEVKF 158
QY 61 NMVYDGVVHNHNAKTRPREQYNSTYRVYSLTVLHQMNMNGKEYCKVSNKALPAPIEKT 120
DB 159 NMVYDGVVHNHNAKTRPREQYNSTYRVYSLTVLHQMNMNGKEYCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTP 180
DB 219 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFELYSKLTVDKSRMOQGNVFCSCVMHEALHNHYQORSLSLSPGK 232
DB 279 PVLDSVGSFELYSKLTVDKSRMOQGNVFCSCVMHEALHNHYQORSLSLSPGK 330

RESULT 15

US-10-269-805-68
; Sequence 68, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-68

Query Match 97.2%; Score 1225; DB 9; Length 330;
Best Local Similarity 97.0%; Pred. No.1.le-85;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKRDTLMISRPEVTQVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKRDTLMISRPEVTQVVDVSHEDPEVKF 158
QY 61 NMVYDGVVHNHNAKTRPREQYNSTYRVYSLTVLHQMNMNGKEYCKVSNKALPAPIEKT 120
DB 159 NMVYDGVVHNHNAKTRPREQYNSTYRVYSLTVLHQMNMNGKEYCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTP 180
DB 219 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFELYSKLTVDKSRMOQGNVFCSCVMHEALHNHYQORSLSLSPGK 232
DB 279 PVLDSVGSFELYSKLTVDKSRMOQGNVFCSCVMHEALHNHYQORSLSLSPGK 330

Search completed: July 15, 2003, 07:17:18
Job time : 20.7984 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:55:24 ; Search time 9.31311 Seconds
(Without alignments)
732.958 Million cell updates/sec

Title: US-09-847-208B-3

Perfect score: 1260

Sequence: 1 EPKSCDKHTHTCPCPAPPELL.....MHEALNHHYQORSLSPGK 232

Scoring table: BIOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 1225 | 97.2 | 232 | 2 | US-08-595-043A-50 |
| 2 | 1225 | 97.2 | 331 | 4 | US-09-178-869-2 |
| 3 | 1225 | 97.2 | 360 | 1 | US-09-180-100-11 |
| 4 | 1225 | 97.2 | 371 | 1 | US-08-236-311-7 |
| 5 | 1225 | 97.2 | 371 | 3 | US-08-457-918-7 |
| 6 | 1225 | 97.2 | 376 | 4 | US-09-180-100-22 |
| 7 | 1225 | 97.2 | 396 | 4 | US-08-784-512-3 |
| 8 | 1225 | 97.2 | 396 | 4 | US-09-176-228-3 |
| 9 | 1225 | 97.2 | 424 | 5 | PCT-US95-03866-12 |
| 10 | 1225 | 97.2 | 424 | 5 | PCT-US95-03866-14 |
| 11 | 1225 | 97.2 | 437 | 5 | PCT-US96-10043-11 |
| 12 | 1225 | 97.2 | 442 | 5 | PCT-US96-10043-9 |
| 13 | 1225 | 97.2 | 446 | 3 | US-08-397-411-7 |
| 14 | 1225 | 97.2 | 449 | 1 | US-08-458-516-13 |
| 15 | 1225 | 97.2 | 459 | 1 | US-08-157-101A-7 |
| 16 | 1225 | 97.2 | 476 | 2 | US-08-378-939-10 |
| 17 | 1225 | 97.2 | 476 | 3 | US-08-487-550-4 |
| 18 | 1225 | 97.2 | 476 | 3 | US-08-487-550-12 |
| 19 | 1225 | 97.2 | 478 | 3 | US-08-487-550-8 |
| 20 | 1220 | 96.8 | 254 | 2 | US-08-284-391B-3 |
| 21 | 1220 | 96.8 | 254 | 4 | US-09-218-950-33 |
| 22 | 1219 | 96.7 | 330 | 4 | US-09-301-593-22 |
| 23 | 1219 | 96.7 | 451 | 2 | US-08-887-352B-14 |
| 24 | 1219 | 96.7 | 451 | 2 | US-08-887-352B-16 |
| 25 | 1219 | 96.7 | 451 | 2 | US-08-887-352B-18 |
| 26 | 1219 | 96.7 | 451 | 2 | US-08-466-151-65 |
| 27 | 1219 | 96.7 | 451 | 4 | US-09-109-207C-14 |

| | | | | | | |
|----|------|------|-----|---|-------------------|-------------------|
| 28 | 1219 | 96.7 | 451 | 4 | US-09-109-207C-16 | Sequence 16, Appl |
| 29 | 1219 | 96.7 | 451 | 4 | US-09-109-207C-18 | Sequence 18, Appl |
| 30 | 1219 | 96.7 | 451 | 4 | US-09-282-505-2 | Sequence 2, Appl |
| 31 | 1219 | 96.7 | 451 | 4 | US-09-054-255-2 | Sequence 2, Appl |
| 32 | 1219 | 96.7 | 451 | 4 | US-09-296-005-14 | Sequence 14, Appl |
| 33 | 1219 | 96.7 | 451 | 4 | US-09-296-005-16 | Sequence 16, Appl |
| 34 | 1219 | 96.7 | 451 | 4 | US-09-296-005-18 | Sequence 18, Appl |
| 35 | 1219 | 96.7 | 452 | 3 | US-09-027-409-71 | Sequence 71, Appl |
| 36 | 1219 | 96.7 | 452 | 4 | US-09-026-985-71 | Sequence 71, Appl |
| 37 | 1219 | 96.7 | 452 | 4 | US-09-121-952A-71 | Sequence 71, Appl |
| 38 | 1219 | 96.7 | 452 | 4 | US-09-234-340A-71 | Sequence 71, Appl |
| 39 | 1219 | 96.7 | 453 | 3 | US-08-466-151-8 | Sequence 8, Appl |
| 40 | 1219 | 96.7 | 453 | 3 | US-08-466-163B-8 | Sequence 8, Appl |
| 41 | 1219 | 96.7 | 453 | 4 | US-09-301-593-18 | Sequence 18, Appl |
| 42 | 1219 | 96.7 | 454 | 2 | US-07-934-373C-22 | Sequence 22, Appl |
| 43 | 1219 | 96.7 | 454 | 3 | US-08-437-642B-22 | Sequence 22, Appl |
| 44 | 1219 | 96.7 | 454 | 4 | US-08-146-206C-22 | Sequence 22, Appl |
| 45 | 1219 | 96.7 | 454 | 5 | PCT-US93-07832-22 | Sequence 22, Appl |

ALIGNMENTS

```
RESULT 1
US-08-595-043A-50
; Sequence 50, Application US/08595043A
; Patent No. 5935824
GENERAL INFORMATION:
APPLICANT: SGARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESSES:
ADDRESS: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: SGAR-00371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO.: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-043A-50

Query Match          97.2%; Score 1225; DB 2; Length 232;
Best Local Similarity 97.0%; Pred. No. 1.1e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLPPLPKDTLMISRTPEVTCVVVDVSHEDPEVK 60
DB 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLPPLPKDTLMISRTPEVTCVVVDVSHEDPEVK 60
QY 61 NMVYGVGVHVNKTKRPREQYNSTYRVYSVLTVLIHQNMNNGEKYCKSNALPAPIKT 120
DB 61 NMVYGVGVHVNKTKRPREQYNSTYRVYSVLTVLIHQNMNNGEKYCKSNALPAPIKT 120

Query Match 97.2%; Score 1225; DB 1; Length 371;
 Best Local Similarity 97.0%; Pred. No. 2.2e-116;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCAPAPELLGSPVFLPPPKPKDTLMSRPREVTCVAVDVSHEDPEYKF 60
 Db 140 EPKSCDKHTHTCPPCAPAPELLGSPVFLPPPKPKDTLMSRPREVTCVAVDVSHEDPEYKF 199
 QY 61 NMVYDGEVHNHAKTKPREEOYNSTYRVSVLTVLHQNMMNGKEKCKVSNKALPAPIEKT 120
 Db 200 NMVYDGEVHNHAKTKPREEOYNSTYRVSVLTVLHQNMMNGKEKCKVSNKALPAPIEKT 259
 QY 121 ISKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTT 180
 Db 260 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTT 319
 QY 181 PVLDSVGSFELYSKLTVDKSRMOQGNVFCSVMHHEALHNHYOQRLSLSPGK 232
 Db 320 PVLDSGSEFLYSKLTVDKSRMOQGNVFCSVMHHEALHNHYOQRLSLSPGK 371

RESULT 5

US-08-457-918-7

Sequence 7, Application US/08457918

Patent No. 6117655

GENERAL INFORMATION:

APPLICANT: Capon, Daniel J.

APPLICANT: Gregory, Timothy J.

TITLE OF INVENTION: Adhesion Variants

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/457,918

FILING DATE: 1-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/236311

FILING DATE: 02-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/936190

FILING DATE: 26-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/842777

FILING DATE: 18-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/250785

FILING DATE: 28-SEP-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/104329

FILING DATE: 02-OCT-1987

ATTORNEY/AGENT INFORMATION:

NAME: Rubinec, Jeffrey S.

REGISTRATION NUMBER: 36,575

REFERENCE/DOCKET NUMBER: P0444P1C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8228

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 371 amino acids

TYPE: amino acid
 TOPOLOGY: linear
 US-08-457-918-7

Query Match 97.2%; Score 1225; DB 3; Length 371;
 Best Local Similarity 97.0%; Pred. No. 2.2e-116;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCAPAPELLGSPVFLPPPKPKDTLMSRPREVTCVAVDVSHEDPEYKF 60
 Db 140 EPKSCDKHTHTCPPCAPAPELLGSPVFLPPPKPKDTLMSRPREVTCVAVDVSHEDPEYKF 199
 QY 61 NMVYDGEVHNHAKTKPREEOYNSTYRVSVLTVLHQNMMNGKEKCKVSNKALPAPIEKT 120
 Db 200 NMVYDGEVHNHAKTKPREEOYNSTYRVSVLTVLHQNMMNGKEKCKVSNKALPAPIEKT 259
 QY 121 ISKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTT 180
 Db 260 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTT 319
 QY 181 PVLDSVGSFELYSKLTVDKSRMOQGNVFCSVMHHEALHNHYOQRLSLSPGK 232
 Db 320 PVLDSGSEFLYSKLTVDKSRMOQGNVFCSVMHHEALHNHYOQRLSLSPGK 371

RESULT 6

US-09-180-100-22

Sequence 22, Application US/09180100

Patent No. 6306395

GENERAL INFORMATION:

APPLICANT: NAKAMURA, No. 630639510

APPLICANT: NAGATA, Shigekazu

TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE

FILE REFERENCE: 1110-207P

CURRENT APPLICATION NUMBER: US/09/180,100

EARLIER FILING DATE: 1998-11-02

EARLIER APPLICATION NUMBER: PCT/JP97/01502

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 22

LENGTH: 376

TYPE: PRT

ORGANISM: Homo sapiens

US-09-180-100-22

Query Match 97.2%; Score 1225; DB 4; Length 376;
 Best Local Similarity 97.0%; Pred. No. 2.2e-116;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCAPAPELLGSPVFLPPPKPKDTLMSRPREVTCVAVDVSHEDPEYKF 60
 Db 145 EPKSCDKHTHTCPPCAPAPELLGSPVFLPPPKPKDTLMSRPREVTCVAVDVSHEDPEYKF 204
 QY 61 NMVYDGEVHNHAKTKPREEOYNSTYRVSVLTVLHQNMMNGKEKCKVSNKALPAPIEKT 120
 Db 205 NMVYDGEVHNHAKTKPREEOYNSTYRVSVLTVLHQNMMNGKEKCKVSNKALPAPIEKT 264
 QY 121 ISKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTT 180
 Db 265 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTT 324
 QY 181 PVLDSVGSFELYSKLTVDKSRMOQGNVFCSVMHHEALHNHYOQRLSLSPGK 232
 Db 325 PVLDSGSEFLYSKLTVDKSRMOQGNVFCSVMHHEALHNHYOQRLSLSPGK 376

RESULT 7

US-08-784-512-3

Sequence 3, Application US/08784512

Patent No. 5872209

GENERAL INFORMATION:

APPLICANT: BARTNIK, Eckart

APPLICANT: EIDENMUELLER, Bernd
APPLICANT: BUETTNER, Frank
APPLICANT: CATERSON, Bruce
APPLICANT: HUGHES, Clare
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: and native aggrecon to study the proteolytic activity of
TITLE OF INVENTION: "Aggreconase" in cell culture systems
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentlin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,512
FILING DATE: 17-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96100682.2
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/311
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..396
US-08-784-512-3

Query Match 97.2%; Score 1225; DB 2; Length 396;
Best Local Similarity 97.0%; Pred. No. 2.4e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCTCPAPPELLGSPVFLFPPKPKDTLMISRTPEYTCVAVDSHEDPEVKF 60
|||||
DB 165 EPKSCDKTHCTCPAPPELLGSPVFLFPPKPKDTLMISRTPEYTCVAVDSHEDPEVKF 224
61 NMVVDGVEVHNATKPREBOYNSTRVSVLTVLHOMWNGKEKCKVSKALPAPIEKT 120
DB 225 NMVVDGVEVHNATKPREBOYNSTRVSVLTVLHOMWNGKEKCKVSKALPAPIEKT 284
QY 121 ISRAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMNSQPENNNKTPP 180
DB 285 ISRAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMNSQPENNNKTPP 344
QY 181 PVLDSVGSFPLYSKLTVDKSRMOOGNVFSCSVMHAEALHNHYOQRSLSLSPGK 232
DB 345 PVLDSVGSFPLYSKLTVDKSRMOOGNVFSCSVMHAEALHNHYOQRSLSLSPGK 396

RESULT 8
US-09-176-228-3
Sequence 3, Application US/09176228
GENERAL INFORMATION:
APPLICANT: BARTNIK, Eckart
APPLICANT: EIDENMUELLER, Bernd

APPLICANT: BUETTNER, Frank
APPLICANT: CATERSON, Bruce
APPLICANT: HUGHES, Clare
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: and native aggrecon to study the proteolytic activity of
TITLE OF INVENTION: "Aggreconase" in cell culture systems
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentlin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/176,228
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/784,512
FILING DATE: 17-JAN-1997
APPLICATION NUMBER: EP 96100682.2
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/311
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..396
US-09-176-228-3

Query Match 97.2%; Score 1225; DB 4; Length 396;
Best Local Similarity 97.0%; Pred. No. 2.4e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCTCPAPPELLGSPVFLFPPKPKDTLMISRTPEYTCVAVDSHEDPEVKF 60
|||||
DB 165 EPKSCDKTHCTCPAPPELLGSPVFLFPPKPKDTLMISRTPEYTCVAVDSHEDPEVKF 224
61 NMVVDGVEVHNATKPREBOYNSTRVSVLTVLHOMWNGKEKCKVSKALPAPIEKT 120
DB 225 NMVVDGVEVHNATKPREBOYNSTRVSVLTVLHOMWNGKEKCKVSKALPAPIEKT 284
QY 121 ISRAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMNSQPENNNKTPP 180
DB 285 ISRAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMNSQPENNNKTPP 344
QY 181 PVLDSVGSFPLYSKLTVDKSRMOOGNVFSCSVMHAEALHNHYOQRSLSLSPGK 232
DB 345 PVLDSVGSFPLYSKLTVDKSRMOOGNVFSCSVMHAEALHNHYOQRSLSLSPGK 396

RESULT 9
PCT-US95-03866-12
Sequence 12, Application PC/TUS9503866
GENERAL INFORMATION:
APPLICANT: CytoMed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)

```
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESSES:
ADDRESS: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cytomed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-03866-12

Query Match          97.2% Score 1225; DB 5; Length 424;
Best Local Similarity 97.0%; Pred. No. 2.7e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRPPEVTCVVVDVSHEDPEVKF 60
DB 193 EPKSCDKHTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRPPEVTCVVVDVSHEDPEVKF 252
QY 61 NMVYDGVGVHNAKTRPREQYNSTYRVYSVLTVFLHQNMMNGKEYCKVSNKALPAPIEKT 120
DB 253 NMVYDGVGVHNAKTRPREQYNSTYRVYSVLTVFLHQNMMNGKEYCKVSNKALPAPIEKT 312
QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTP 180
DB 313 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTP 372
QY 181 PVLDSVGSFFLYSKLTVDKSRMQQGNVSCSYMHGALHNHYQKSLSPGK 232
DB 373 PVLDSVGSFFLYSKLTVDKSRMQQGNVSCSYMHGALHNHYQKSLSPGK 424

RESULT 10
PCT-US95-03866-14
Sequence 14, Application PC/TUS9503866
GENERAL INFORMATION:
APPLICANT: Cytomed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
```

```
STATE: New York
COUNTRY: United States of America
ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cytomed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-03866-14

Query Match          97.2% Score 1225; DB 5; Length 424;
Best Local Similarity 97.0%; Pred. No. 2.7e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRPPEVTCVVVDVSHEDPEVKF 60
DB 193 EPKSCDKHTHTCPPCAPPELLGGPSVFLFPPPKKDTLMISRPPEVTCVVVDVSHEDPEVKF 252
QY 61 NMVYDGVGVHNAKTRPREQYNSTYRVYSVLTVFLHQNMMNGKEYCKVSNKALPAPIEKT 120
DB 253 NMVYDGVGVHNAKTRPREQYNSTYRVYSVLTVFLHQNMMNGKEYCKVSNKALPAPIEKT 312
QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTP 180
DB 313 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTP 372
QY 181 PVLDSVGSFFLYSKLTVDKSRMQQGNVSCSYMHGALHNHYQKSLSPGK 232
DB 373 PVLDSVGSFFLYSKLTVDKSRMQQGNVSCSYMHGALHNHYQKSLSPGK 424

RESULT 11
PCT-US96-10043-11
Sequence 11, Application PC/TUS9610043
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
```

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,213
FILING DATE: 14-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 00786/284001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10043-11

Query Match 97.2%; Score 1225; DB 5; Length 437;
Best Local Similarity 97.0%; Pred. No. 2.8e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHNCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 206 EPKSCDKTHNCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 265
QY 61 NMVYDGEVHNHAKTKPREEOYNSTYRVVSVLTVLIHQMMNGKEYCKVSKALPAPIEKT 120
DB 266 NMVYDGEVHNHAKTKPREEOYNSTYRVVSVLTVLIHQMMNGKEYCKVSKALPAPIEKT 325
QY 121 ISKAKVQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMWESNGOPENNYKTTTP 180
DB 326 ISKAKGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMWESNGOPENNYKTTTP 385
QY 181 PVLDSVGSFELYSKLTVDKSRMOQGNVSCSVMHREALHNHYOQRSLSISPGK 232
DB 386 PVLDSVGSFELYSKLTVDKSRMOQGNVSCSVMHREALHNHYOQRSLSISPGK 437

RESULT 12
PCT-US96-10043-9
Sequence 9, Application PC/TUS9610043
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,213
FILING DATE: 14-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Lech, Karen F.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 00786/284001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10043-9

Query Match 97.2%; Score 1225; DB 5; Length 442;
Best Local Similarity 97.0%; Pred. No. 2.8e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHNCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 211 EPKSCDKTHNCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 270
QY 61 NMVYDGEVHNHAKTKPREEOYNSTYRVVSVLTVLIHQMMNGKEYCKVSKALPAPIEKT 120
DB 271 NMVYDGEVHNHAKTKPREEOYNSTYRVVSVLTVLIHQMMNGKEYCKVSKALPAPIEKT 330
QY 121 ISKAKVQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMWESNGOPENNYKTTTP 180
DB 331 ISKAKGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMWESNGOPENNYKTTTP 390
QY 181 PVLDSVGSFELYSKLTVDKSRMOQGNVSCSVMHREALHNHYOQRSLSISPGK 232
DB 391 PVLDSVGSFELYSKLTVDKSRMOQGNVSCSVMHREALHNHYOQRSLSISPGK 442

RESULT 13
US-08-397-411-7
Sequence 7, Application US/08397411
Patent No. 6129914
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: TSO, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-411-7

Query Match 97.2%; Score 1225; DB 3; Length 446;
Best Local Similarity 97.0%; Pred. No. 2.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 215 EPKSDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 274
QY 61 NMVYDGEVHNWKTREEOYNSTYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120
DB 275 NMVYDGEVHNWKTREEOYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKT 334
QY 121 ISKAKVQREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTP 180
DB 335 ISKAKGPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTP 394
QY 181 PVLDSVGSFELYSKLTVDKSRMOGNVFSCVMHEALHNHYOQSLSLSPGK 232
DB 395 PVLDSGSEFLYSLKLTVDKSRMOGNVFSCVMHEALHNHYOQSLSLSPGK 446

RESULT 14
US-08-458-516-13

Sequence 13, Application US/08458516
Patent No. 5777085

GENERAL INFORMATION:

APPLICANT: Co, Man Sung

APPLICANT: Tso, J. Yun

TITLE OF INVENTION: Humanized Antibodies Reactive with

TITLE OF INVENTION: GrIIb/IIIA

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith

STREET: One Market Plaza, Stewart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/458,516

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/059,159

FILING DATE: 03-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-37-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 449 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-13

Query Match 97.2%; Score 1225; DB 1; Length 449;
Best Local Similarity 97.0%; Pred. No. 2.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 218 EPKSDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 277
QY 61 NMVYDGEVHNWKTREEOYNSTYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120
DB 278 NMVYDGEVHNWKTREEOYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKT 337
QY 121 ISKAKVQREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTP 180
DB 338 ISKAKGPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTP 397
QY 181 PVLDSVGSFELYSKLTVDKSRMOGNVFSCVMHEALHNHYOQSLSLSPGK 232
DB 398 PVLDSGSEFLYSLKLTVDKSRMOGNVFSCVMHEALHNHYOQSLSLSPGK 449

RESULT 15
US-08-157-101A-7

Sequence 7, Application US/08157101A
Patent No. 5808032

GENERAL INFORMATION:

APPLICANT: KURIHARA, TATSUYA

APPLICANT: MATSUKURA, SHIGEKAZU

APPLICANT: TSUBOKA, NOBUO

APPLICANT: ARIMA, KENJI

APPLICANT: NISHIHARA, TATSURO

TITLE OF INVENTION: ANTI-BBS ANTIBODY GENES AND EXPRESSION

TITLE OF INVENTION: PLASMIDS THEREFOR

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: PILLSBURY, MADISON & SUTRO

STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/157,101A

FILING DATE: 05-APR-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: TITUS, MARILAN K

REGISTRATION NUMBER: 35843

REFERENCE/DOCKET NUMBER: 9437/204199

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3711

TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 459 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-157-101A-7

Query Match 97.2%; Score 1225; DB 1; Length 459;
Best Local Similarity 97.0%; Pred. No. 3e-116;

| | Matches | 225; | Conservative | 3; | Mismatches | 4; | Indels | 0; | Gaps | 0; |
|----|---------|---|--------------|----|------------|----|--------|----|------|----|
| OY | 1 | EPKSCDKTHTCPCPCPAPELLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF | 60 | | | | | | | |
| Db | 228 | EPKSCDKTHTCPCPCPAPELLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF | 287 | | | | | | | |
| OY | 61 | NWYVDGVEVHNAVKTRPREEOYNSTYRVSVLTVLHÖNMNGKEYKCKVSNKALPAPIEKT | 120 | | | | | | | |
| Db | 288 | NWYVDGVEVHNAVKTRPREEOYNSTYRVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKT | 347 | | | | | | | |
| OY | 121 | ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPP | 180 | | | | | | | |
| Db | 348 | ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPP | 407 | | | | | | | |
| OY | 181 | PVLDSVGSFFLYSKLTYDKSRMOQGNVFSQSVMHGALHNHYOQRSLSISPGK | 232 | | | | | | | |
| Db | 408 | PVLDSVGSFFLYSKLTYDKSRMOQGNVFSQSVMHGALHNHYTKSLSISPGK | 459 | | | | | | | |

Search completed: July 15, 2003, 07:02:38
 Job time : 11.3131 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: July 15, 2003, 06:52:29 ; Search time 18.549 Seconds
(without alignments)
1657.949 Million cell updates/sec

Title: US-09-847-208b-6

Perfect score: 1707

Sequence: 1 FTPTVKILSSCDGGGHP.....HEASPSQTVQRAVSNPGK 320

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 1707 | 100.0 | 428 | 1 EHHU | Ig epsilon chain C |
| 2 | 1644.5 | 96.3 | 426 | 1 I36948 | Ig epsilon chain C |
| 3 | 793 | 46.5 | 429 | 1 EHRT | Ig epsilon chain C |
| 4 | 751 | 44.0 | 388 | 1 EHMS | Ig epsilon chain C |
| 5 | 678.5 | 39.7 | 423 | 1 EHMS | Ig epsilon chain C |
| 6 | 576 | 33.7 | 227 | 1 PH1215 | Ig epsilon chain C |
| 7 | 576 | 33.7 | 227 | 1 PH1215 | Ig epsilon chain C |
| 8 | 570 | 33.4 | 115 | 2 E51116 | Ig epsilon chain C |
| 9 | 471 | 27.6 | 572 | 2 B46529 | Ig epsilon chain C |
| 10 | 471 | 27.6 | 572 | 2 B46529 | Ig epsilon chain C |
| 11 | 470 | 27.5 | 433 | 3 S31436 | Ig epsilon chain C |
| 12 | 469 | 27.5 | 504 | 2 S00390 | Ig epsilon chain C |
| 13 | 455.5 | 26.7 | 549 | 2 S04845 | Ig epsilon chain C |
| 14 | 439.5 | 25.7 | 455 | 1 MHMS | Ig epsilon chain C |
| 15 | 439.5 | 25.7 | 455 | 2 A24976 | Ig epsilon chain C |
| 16 | 433 | 25.4 | 328 | 2 I47158 | Ig epsilon chain C |
| 17 | 430.5 | 25.2 | 476 | 1 MHMS | Ig epsilon chain C |
| 18 | 428.5 | 25.1 | 454 | 1 MHMS | Ig epsilon chain C |
| 19 | 428 | 25.1 | 328 | 1 I47161 | Ig epsilon chain C |
| 20 | 416 | 24.4 | 326 | 1 G2HU | Ig epsilon chain C |
| 21 | 415 | 24.3 | 328 | 2 I47159 | Ig epsilon chain C |
| 22 | 414 | 24.3 | 444 | 2 PC4436 | Ig epsilon chain C |
| 23 | 413.5 | 24.2 | 457 | 2 S03961 | Ig epsilon chain C |
| 24 | 413 | 24.2 | 453 | 2 S37768 | Ig epsilon chain C |
| 25 | 412 | 24.1 | 328 | 2 I47160 | Ig epsilon chain C |
| 26 | 411.5 | 24.1 | 470 | 2 S22080 | Ig epsilon chain C |
| 27 | 410 | 24.0 | 391 | 1 MHMS | Ig epsilon chain C |
| 28 | 409.5 | 24.0 | 343 | 2 S25644 | Ig epsilon chain C |
| 29 | 409 | 24.0 | 592 | 2 S25705 | Ig epsilon chain C |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 405.5 | 23.8 | 458 | 1 MHRB | Ig mu chain C regi |
| 31 | 404.5 | 23.7 | 329 | 1 G2GP | Ig gamma-2 chain C |
| 32 | 404 | 23.7 | 474 | 2 S15590 | Ig heavy chain - h |
| 33 | 402.5 | 23.6 | 452 | 1 MHMS | Ig mu chain C regi |
| 34 | 402 | 23.6 | 324 | 1 G1MS | Ig gamma-1 chain C |
| 35 | 400.5 | 23.5 | 277 | 2 I47162 | Ig gamma-1 chain C |
| 36 | 399 | 23.4 | 330 | 1 G2MSA | Ig gamma-2a chain |
| 37 | 399 | 23.4 | 469 | 2 S37483 | Ig gamma-2a chain |
| 38 | 398 | 23.3 | 446 | 2 S40295 | Ig gamma-2a chain |
| 39 | 397.5 | 23.3 | 330 | 1 G2HU | Ig gamma-1 chain C |
| 40 | 397 | 23.3 | 393 | 1 G1MS | Ig gamma-1 chain C |
| 41 | 396.5 | 23.2 | 479 | 1 MHRB | Ig mu chain C regi |
| 42 | 396.5 | 23.2 | 627 | 2 S14683 | Ig mu chain precu |
| 43 | 396 | 23.2 | 475 | 2 S01321 | Ig gamma-2b chain |
| 44 | 395.5 | 23.2 | 472 | 2 S1459 | Ig gamma-1 chain |
| 45 | 394 | 23.1 | 399 | 1 G2MSM | Ig gamma-2a chain |

ALIGNMENTS

RESULT 1

EHMU
Ig epsilon chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C:Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116;
R:Flanagan, J.G.; Rabbits, T.H.
EMBO J. 1, 655-660, 1982
A:Title: The sequence of a human immunoglobulin epsilon heavy chain constant region 9
A:Reference number: A22771; MUID:84236029; PMID:6234164
A:Accession: A22771
A:Molecule type: DNA
A:Residues: 1-428 <F1A>
A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:q185035
R:Ueda, S.; Nakai, S.; Nishida, Y.; Hasejima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
A:Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseu
A:Reference number: A23195; MUID:84207910; PMID:6327276
A:Accession: A23195
A:Molecule type: DNA
A:Residues: 2-428 <UED>
A:Cross-references: GB:J00222; NID:q184755
R:Zhang, K.; Saxon, A.; Max, E.E.
J. Exp. Med. 176, 298-304, 1992
A:Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splic
A:Reference number: PH1214; MUID:92308839; PMID:1613458
A:Accession: PH1214
A:Molecule type: DNA
A:Residues: 320-428 <ZHA>
A:Cross-references: EMBL:X63693; GB:S38668; NID:932987
R:Seno, M.; Kurokawa, T.; Ono, Y.; Ono, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; S
Nucleic Acids Res. 11, 719-726, 1983
A:Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon
A:Reference number: A93491; MUID:83168897; PMID:6300763
A:Accession: A93491
A:Molecule type: mRNA
A:Residues: 1-428 <SEN>
A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:q185035
R:Max, E.E.; Batley, J.; Ney, R.; Kirsch, I.R.; Leder, P.
Cell 29, 691-699, 1982
A:Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A:Reference number: A90824; MUID:83001945; PMID:6288268
A:Accession: A90824
A:Molecule type: DNA
A:Residues: 1-358, 'L', 360-428 <MAX>
A:Cross-references: GB:J00222; NID:q184755
R:Benichou, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.
A:Reference number: A94418
A:Accession: A94418
A:Molecule type: protein

A:Residues: 'GAWTL',6,'X',8-16,'B',18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L',14
 A:Experimental source: myeloma protein Nd
 R:Kerten, J.H.; Molgaard, H.V.; Houghon, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
 Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
 A:Title: Cloning and sequence determination of the gene for the human immunoglobulin eps
 A:Reference number: A93933; MUID:83065234; PMID:6815656
 A:Accession: B93933
 A:Molecule type: mRNA
 A:Residues: 1-40:68-114;427-428 <KEN>
 A:Cross-references: GB:100022; NID:g185035
 R:Ikemura, S.
 FEBS Lett. 224, 306-310, 1987
 A:Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragmen
 A:Reference number: S02438; MUID:86083554; PMID:3121387
 A:Accession: S02438
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 98-352 <IKE>
 R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
 J. Biol. Chem. 269, 456-462, 1994
 A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
 A:Reference number: A53116; MUID:94103254; PMID:8276835
 A:Accession: A53116
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 320-428 <ZH2>
 A:Experimental source: myeloma U266-derived cell line AF-10
 A:Note: sequence extracted from NCBI backbone (NCBI:141701, NCBIP:141702)
 R:Hellman, L.
 Eur. J. Immunol. 23, 159-167, 1993
 A:Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of
 A:Reference number: A46536; MUID:93122085; PMID:8419166
 A:Accession: C46536
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 382-426 <HEU>
 A:Cross-references: GB:S55273; NID:g263166; PIDN:AMB24857.1; PID:g263167
 A:Experimental source: B cell myeloma U-266
 A:Note: sequence extracted from NCBI backbone (NCBIP:125297)
 A:Accession: D46536
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 382-391 <HE2>
 A:Cross-references: GB:S55276; NID:g263168; PIDN:AMB24858.1; PID:g263169
 A:Experimental source: B cell myeloma U-266
 A:Note: sequence extracted from NCBI backbone (NCBIP:125299)
 A:Accession: A46536
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 401-428 <HE3>
 A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
 A:Experimental source: B cell myeloma U-266
 A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
 C:Genetics:
 A:Gene: GDB:IGHE
 A:Cross-references: GDB:119335; OMIM:147180
 A:Map position: 14q32.33-14q32.33
 A:Introns: 1/1; 104/1; 211/1; 319/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (K)
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
 F:22-87/Domain: immunoglobulin homology <IM1>
 F:128-195/Domain: immunoglobulin homology <IM2>
 F:232-301/Domain: immunoglobulin homology <IM3>
 F:338-407/Domain: immunoglobulin homology <IM4>
 F:14/Disulfide bonds: interchain (to light chain) #status predicted
 F:15-105-29-85-133-193,239-299,345-405/Disulfide bonds: #status predicted
 F:21,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:121,209/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 100.0%; Score 1707; DB 1; Length 426;
 Best Local Similarity 100.0%; Pred. No. 8.1e-120;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTTPPTVKILQSSCGGCHFPPTIQLCLVSGTPTGTTITWLEDGQVMDVLDSTASTQOE 60
 109 FTTPPTVKILQSSCGGCHFPPTIQLCLVSGTPTGTTITWLEDGQVMDVLDSTASTQOE 168
 QY 61 GELASTOSELTLSOKHMLSDRTYTCQVYTGCHTFEDSTKCADSNPGRVSAIYLRSPSPFD 120
 169 GELASTOSELTLSOKHMLSDRTYTCQVYTGCHTFEDSTKCADSNPGRVSAIYLRSPSPFD 228
 Db 121 LFIKSPITICLVVDLAPSKGTVNLTWRSRAGKRVNHNSTRKEEKORNGTTLVSTLPVGT 180
 Db 229 LFIKSPITICLVVDLAPSKGTVNLTWRSRAGKRVNHNSTRKEEKORNGTTLVSTLPVGT 288
 QY 181 RDMIEGETYOCRVTHPHLPALMSTRTKTSGRAPAEVYAFATPEWPGSRDKRTLACLIQ 240
 289 RDMIEGETYOCRVTHPHLPALMSTRTKTSGRAPAEVYAFATPEWPGSRDKRTLACLIQ 348
 Db 241 NFMPEDISVQVLLHNEVOLPDARHSTTOPRKTKSGGFVFSRLVETRAWEQKDEFTICRAV 300
 349 NFMPEDISVQVLLHNEVOLPDARHSTTOPRKTKSGGFVFSRLVETRAWEQKDEFTICRAV 408
 QY 301 HEAPSPOTVORAVSNPGR 320
 Db 409-HEAPSPOTVORAVSNPGR 428

RESULT 2

Ig epsilon-chain - chimpanzee (fragment)
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 04-Oct-1996 #sequence revision 04-Oct-1996 #text-change 21-Jan-2000
 C:Accession: 136948
 R:Sakoyama, Y.; Hong, K.
 Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
 A:Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orang
 A:Reference number: 136948; MUID:87147196; PMID:3103123
 A:Accession: 136948
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-426 <RES>
 A:Cross-references: GB:M15398; NID:g176797; PIDN:AAA35416.1; PID:g176798
 C:Genetics:
 A:Introns: 103/1; 209/1; 317/1
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:336-405/Domain: immunoglobulin homology <IMM>

Query Match 96.3%; Score 1644.5; DB 2; Length 426;
 Best Local Similarity 97.2%; Pred. No. 3.7e-115;
 Matches 311; Conservative 3; Mismatches 5; Indels 1; Gaps 1;
 QY 1 FTTPPTVKILQSSCGGCHFPPTIQLCLVSGTPTGTTITWLEDGQVMDVLDSTASTQOE 60
 108 FTTPPTVKILQSSCGGCHFPPTIQLCLVSGTPTGTTITWLEDGQVMDVLDSTASTQOE 166
 Db 108 FTTPPTVKILQSSCGGCHFPPTIQLCLVSGTPTGTTITWLEDGQVMDVLDSTASTQOE 166
 QY 61 GELASTOSELTLSOKHMLSDRTYTCQVYTGCHTFEDSTKCADSNPGRVSAIYLRSPSPFD 120
 167 GELASTOSELTLSOKHMLSDRTYTCQVYTGCHTFEDSTKCADSNPGRVSAIYLRSPSPFD 226
 Db 121 LFIKSPITICLVVDLAPSKGTVNLTWRSRAGKRVNHNSTRKEEKORNGTTLVSTLPVGT 180
 Db 229 LFIKSPITICLVVDLAPSKGTVNLTWRSRAGKRVNHNSTRKEEKORNGTTLVSTLPVGT 286
 QY 181 RDMIEGETYOCRVTHPHLPALMSTRTKTSGRAPAEVYAFATPEWPGSRDKRTLACLIQ 240
 287 RDMIEGETYOCRVTHPHLPALMSTRTKTSGRAPAEVYAFATPEWPGSRDKRTLACLIQ 346
 Db 241 NFMPEDISVQVLLHNEVOLPDARHSTTOPRKTKSGGFVFSRLVETRAWEQKDEFTICRAV 300
 347 NFMPEDISVQVLLHNEVOLPDARHSTTOPRKTKSGGFVFSRLVETRAWEQKDEFTICRAV 406
 QY 301 HEAPSPOTVORAVSNPGR 320
 Db 409-HEAPSPOTVORAVSNPGR 428


```

QY      12  ITFLVYDLAPSGITVALJLMSRASGKPVNHSRKEEKQNGLYLSTLPATGRWIEGT 168
      Db      358  LITLVYDLESEK--NNAVITNDECKTISVASQMTYTKHHNNATTTSTSLPVYAKWDIEGYG 416
QY      189  YQCRVTHPHPLPALMKSTYTKTSGPRAAEVYUAFALPEWPGSRDRITLACIONEMPEDIS 248
      Db      417  YQCIYVHPPEPFPRIYVSIKTKPGQSAEYVVFPEPE--EESEDKRTLTCLIQNFFPEDIS 475
QY      249  VQMLHNEVQDLPAKHSSTQPKTKKS--GFVFSKLEYTRAEWQCKDEFLICRAVHEAASP 306
      Db      476  VQMLGSGKILSNSQHSHTPTLTKSNSGNGEFLFSRLYVAKTLMTQROKTCOVITHEALOK 535
QY      307  SQTQVRAVSVN 317
      Db      536  PKLEKTIISTS 546

```

RESULT 6

Ig epsilon chain C region (version 2) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
 C:Accession: A02145
 R:ishida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo, T.
 EMBO J. 1, 1117-1123, 1982
 A:Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison with the DNA of the lambda and gamma genes
 A:Reference number: A90966; MUID:84236092; PMID:6329728
 A:Accession: A02145
 A:Molecule type: DNA
 A:Residues: 1-423 <ISH>
 A:Note: the sequence was determined from the germ-line gene
 C:Genetics:
 A:Introns: 91/1; 199/1; 307/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
 C:Superfamily: Immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:16-77/Domain: immunoglobulin homology <IM1>
 F:115-183/Domain: immunoglobulin homology <IM2>
 F:220-288/Domain: immunoglobulin homology <IM3>
 F:335-396/Domain: immunoglobulin homology <IM4>
 F:23-75,122-181,227-286,332-394/Disulfide bonds: #status predicted
 F:34,84,167,239,262,417/Binding site: carbohydrate (Asn) (covalent) #status predicted

| | | | | |
|---------------------------|-------|--------------------|-----------|-------------|
| Query Match | 39.7% | Score 678.5; | DB 1. | Length 423; |
| Best Local Similarity | 43.7% | Pred. No. 3.7e-43; | | |
| Matches 136; Conservative | 56; | Mismatches 112; | Indels 7; | Gaps 6 |

| | | | |
|----|-----|---|-----|
| QY | 13 | CGGGGFFPRTDILCLVSGVTPGGTINIMV-EDCGVMDVUDLSTASTQOEELASTOSELT | 71 |
| | | | |
| Db | 109 | CPRNA-FHSTIQLYCFYGHILINDVSWMLMDREIDTDLAQVLYLKEEBKLASTOSKLN | 167 |
| QY | 72 | LSQKMLSDRTYTCQVYVQGHTEFDESTYKCKADSNPRGVSAVLSPSPFDLFIKSPPTTC | 131 |
| | | | |
| Db | 168 | ITEQOMNSSTTCRYTSQGVADYLAHTEPCRDHERGATVYLTPPSLDLIDYONGAKRLTC | 227 |
| QY | 132 | LVVDLAPSKGYNLMTWSRASKRPVNHSTRKEEKOENGLIYVSTLPYGTBDWTEGEGYOC | 191 |
| | | | |
| Db | 228 | LVVDESEK-NVNTVMQEKTSVSASQWTKHNHNNATTSITSLPVVADMDIEGYGOC | 286 |
| QY | 192 | RYTHNPLRALMRSTTKTS-GRPARPYUATATBEWGSBPKRLACLIONFREDISVQ | 250 |
| | | | |
| Db | 287 | WLDNRPFRPRLYKSTLTPQVSOBSAPAEVYVPRPE-ESESEKRLTLLIONFREDISVQ | 345 |
| QY | 251 | MLHNEVOLRPAHSTTQPRKTKG--GFVFSRLVYTRAEWOKDEICRAVHEAASPQ | 308 |
| | | | |
| Db | 346 | WLGDGKLISNOSHSTTPELKSNGSQGFFIRSLVEAKLMTLOKQCYTCQVINEALQKPR | 405 |
| QY | 309 | TYQRAVSYPNG | 319 |
| | | | |
| Db | 406 | KLEKTIISTISLG | 416 |

RESULT 7
PH1215
Ig epsilon chain C region form 2 - human (fragment)
D:\biosci\home\craig\craig\...

RESULT 7

C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C:Accession: PH1215
J:Zhang, K.; Saxon, A.; Max, E.E.
J. Exp. Med. 176, 233-243, 1992
A:Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing
A:Reference number: PH1214, MUID:92308839, PMID:1613458
A:Accession: PH1215
A:Molecule type: DNA
A:Residues: 1-227 <ZHA>
A:Cross-references: EMBL:X63693
C:Genetics:
A:Initons: 108/1; 200/3
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; immunoglobulin
F:19-88/Domain: immunoglobulin homology <ITM>

Query Match
Best Local

| | | | | |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match | 33.7%; | Score 576; | DB 2; | Length 227; |
| Best Local Similarity | 100.0%; | Pred. No. 7.7e-36; | | |
| Matches 108; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0 |

DQ 212 PRAAEVYAFATPEWPGSRDKRTLACLIQNMPEDISVQWLHNEVQLPDARHSITQPRT 27
| | | | |
DY 1 PRAAEVYAFATPEWPGSRDKRTLACLIQNMPEDISVQWLHNEVQLPDARHSITQPRT 60

QY 272 KSGGFVFSRLVTRAEMQKDEFICRAVHEASPSQTQRAVSVNPG 319
 |||||
 Db 61 KSGGFVFSRLVTRAEMQKDEFICRAVHEASPSQTQRAVSVNPG 108

RESULT 8

Iq eps

Ig epsilon chain C region form 3 - human (fragment)
 N:Alternate names: Ig epsilon chain C region, membrane-bound form (clone CH4-M2')
 C:Species: Homo sapiens (man)

C:\date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #ext_change 21-Jan-2000
C:\Accession: PH1216; D53116
B:\change K : Gayon A : May F F

Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing
Author(s): Zhang, N., Sakai, A., Max, E.E.
J. Exp. Med. 176, 233-243, 1992

A/Reference number: PH1214; MUID:92308839; PMID:16134588
A/Accession: PH1216

A;Molecule type: DNA
A;Residues: 1-243 <ZHA>

A; Cross-references: EMBL:X63693
R; Zhang, K.; Max, E.E.; Chéah, H.K.; Saxon, A

A/Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produced by B101. Chem 269, 456-462, 1994

A;Accession: D53116
A;Reference Number: A53110; MUID:94103234; PMID:82/6833
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-243 <ZH

A; Experimental source: myeloma U266-derived cell line AF-10
A; Note: sequence extracted from NCBI backbone (NCBIN:141701)

C;Genetics:
A;Introns: 108/1

C:Superfamily; immunoglobulin C region; immunoglobulin
C:keywords: alternative splicing; immunoglobulin

Query Match 33 79! Score 576!
F;19-88/Domain: Immunoglobulin homology <1MM>

BEST LOCAL
Matches 10

| 212 | PRAPEVVAFAATPEWPGSRDKRTIACLIQNEPDISVOMLHNEVOLPDARHSTTOPRKT | 271 |
|-----|--|-----|
| 00 | 00 | 00 |
| 01 | 01 | 01 |
| 02 | 02 | 02 |
| 03 | 03 | 03 |
| 04 | 04 | 04 |
| 05 | 05 | 05 |
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| 42 | 42 | 42 |
| 43 | 43 | 43 |
| 44 | 44 | 44 |
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| 46 | 46 | 46 |
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| 48 | 48 | 48 |
| 49 | 49 | 49 |
| 50 | 50 | 50 |
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| 90 | 90 | 90 |
| 91 | 91 | 91 |
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| 93 | 93 | 93 |
| 94 | 94 | 94 |
| 95 | 95 | 95 |
| 96 | 96 | 96 |
| 97 | 97 | 97 |
| 98 | 98 | 98 |
| 99 | 99 | 99 |

```

1 PRAPEVAFATPEMPGSRDKRTLACTIONMPEDISVQWLHNEVQLPDARSTTOPKKT 60

```

QY 272 KSGGFVFSLEVTTRAWECKDEFICRAVHAASPSQTVQRAVSVNPG 319
|||||
Db 61 KSGGFVFSRLVETTRAWECKDEFICRAVHAASPSQTVQRAVSVNPG 108

RESULT 9
E53116

I g epsilon chain C region, secreted splice form (clone CH4-3 (UT-CH5-M2')) - human (frag
 C:Species: Homo sapiens (man)
 C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: E53116
 R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
 J. Biol. Chem. 269, 456-462, 1994
 A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
 A:Reference number: A53116; MUID:94103254; PMID:8276835
 A:Accession: E53116
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-115 <ZNA>
 A:Experimental source: myeloma U266-derived cell line AF-10
 A:Note: Sequence extracted from NCBI database (NCBIN:141701, NCBIN:141711, NCBIN:141720)
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:19-88/Domain: immunoglobulin homology <IM>

| | | | | |
|-----------------------|----------------|--------------|----------|------------|
| Query Match | 33.4% | Score 570 | DB 2 | Length 115 |
| Best Local Similarity | 100.0% | Pred. NC | 9.4e-36 | |
| Matches 107 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |

[illegible]

QY 272 KSGGFVFSRL EYTRAEWEQKDFICRAVHEAASPSQT VQRAVSVP 318
 |||||
Db 61 KSGGFFVFSRL EYTRAEWEQKDFICRAVHEAASPSQT VQRAVSVP 107

RESULT 10

Ig Y heavy chain (7.85) - duck
 N.Alternate names: Ig gamma chain (7.8S)
 C.Species: Anas platyrhynchos (domestic duck)
 C.Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
 C.Accession: B46529; S20759
 J.Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
 J. Immunol. 149, 2627-2633, 1992
 A.Title: Structural relationship between the two Igy of the duck, Anas platyrhynchos.
 A.Reference number: A46529; MUID:93017865; PMID:1401901
 A.Accession: B46529
 A.Status: Preliminary
 A.Molecule type: mRNA
 A.Residues: 1-572 <MAG>
 A.Cross-references: EMBL:X65219; NID:G62442; PIDN:CAA6322.1; PID:G62443
 A.Experimental source: spleen
 A.Note: sequence extracted from NCBI backbone (NCBIP:116127)
 C.Superfamily: immunoglobulin C region; immunoglobulin homology
 C.Keywords: Immunoglobulin
 E:37-120/Domain: immunoglobulin homology <IMM>

| | | | | |
|-----------------------|-----------------|-------------------|-----------|------------|
| Query Match | 27.68 | Score 471 | DB 2 | Length 572 |
| Best Local Similarity | 32.08 | Pred. No. 1.6e-27 | | |
| Matches 106 | Conservative 66 | Mismatches 141 | Indels 18 | Gaps 10 |

```

QY      2  TRPKKILQSS-CDGGGHPPTIQLLCLVSGTTPGTINITWLEDGQWMDVDLSTASTIQE 60
      ||| ::| || | | ::|||::|::| | | | :
Db     248  TRPEYQVLHSSVCSLFG--DDSVELLCAVITGSSPPVEVEWLVDS--APAHLYATMTMRQ 303

```

QY 61 GELAS-----TQSELTLSQKHWLSDRTYTCQVY--QGHTFEDSTKCCADSNPRG---VSA 1111

Db 304 REAGSKTYMATSQTNVSRREDWKAGKAFTCRVKHPATGTAQGHARFCPSGAQSCSPIQI 363

QY 112 YLSRSPFDLEIRKSPITTCVLVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLT 171

```

Db      364  FVVPBPSFGSLITQDQAKVHCLVYVNL-PSDASISISWTEKSGALKPDPMLTTEHFNTFTT
Oy      172  VTSTLPGRTDRIEGEGETYOCCRVYTHPLPLPALMRSTTKSGPRAAEVYAFATPMPGSRD
Db      423  ASSSLAISTDMDLAGRFCTVOHEDLVPPLKCSSTAKAGKYATAVITTPPAAEELSLA
Oy      232  KRTIACLIQFMPEDEDSYOMLNHEVOLDPARASTOP-RKTKGSG-FFVFSRLVTRAEW
Db      483  EVITLCLVRGFQPEHVEVOMLRNHNHNSVPAAEVTTPLPKEPNGDSTFFLYSKMTVPKASW
Oy      290  EOKDEFICRAVHEAASPSQTVRAAVSVPNG 320
Db      543  QGGSVSTACMVVHEGL-PMRFQRPDLQKTGK 572

```

RESULT 11
S31436

Ig upslon chain - axolotl (fragment)
 C:Species: Ambystoma mexicanum (axolotl)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999
 C:Accession: S31436
 R:Feilhan, J.S.; Miles, M.V.; Schwager, J.; Charlemagne, J.
 submitted to the EMBL Data Library, November 1992
 A:Description: cDNA sequence of Ambystoma mexicanum upslon heavy Igy chain
 A:Reference number: S31436
 A:Accession: S31436
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-433 <FEEL>
 A:Cross-references: EMBL:X69492; NID:g62420; PID:g62421
 C:Superfamily: Immunoglobulin C region, Immunoglobulin homology

| | | | | |
|---------------------------|-------|--------------------|------------|-------------|
| Query Match | 27.5% | Score 470; | DB 2; | Length 433; |
| Best Local Similarity | 31.0% | Pred. No. 1.3e-27; | | |
| Matches 102; Conservative | 72; | Mismatches 137; | Indels 18; | Gaps 9 |

```
QY      4 PTVKLIQSSC---DGGGHPPTIQLCLVSGTPTGINTITWEDGQVNDVDLSTASTQOE 60
        |:|::||| | | :||:|||| | : ||: | : :
Db      111 PSQVLQSSCADTDGNG---SIELVCISGTPDNINQVRWLVDNKMALPIQGTSPPQKD 166
```

```

QY      61 GE-LASTQSELTLSQKHWLSDRTYTCQVYQCHT--FEDSTKCADS-NPRGVSATYLSRP 116
      | : | : : : | | : | : : | : | : | : | : | : | : | : | : | : |
Db      167 GQGTFSTTSQINVTKSDWASGDKYTCQVEHNPATSSRABDTINHCCADSQTPYQKVFLLAP 220

```

```
QY      117 SPEDLEIRKSTITCLVVDLAPSKGYNLNWRASGCPVNHSRKKEQRNGTLTVTSL 176
       ||::|::||:|::|||::|::||:|::|||::|::||:|::|||::|::||:|::|||::|::||:
Db     227 KARDLYIANQPVICIKTKMENS-DSLSVTWKRREGDEAAVISQYLIDSDGTFTAMSYL 285
```

QY 177 PVGTRDMEIETGYQCRKTHPHPLRALMRSTVTSGPRAAPEVYAFATLEMP-GSRDKRTL 235

Db 286 NITKNEMERGEFTCKKKHFDLPPLSRVSVKPTGRSFAPITMVVFAPHEMELANYDFVSL 345

QY 236 ACLIQNMPEDISVQMLHNEQLPDRARHTTPRKTYGSG-----FFVFSRLEYTRAEMEQ 29

Db 346 TCLVNSFSPDDIYIQMKQGKSVIPSDKYVSMPRQEAAGTAGLGTTFYSMLPTIQKSDMDK 40

```

QY      292 KDEFCIRAVHEAASPSQTVQRAVSYPGK 320
          ::||| | | : | : ||
Db      406 RETFTCVAAHSASV-PKMLMTRRIQKPLGK 433

```

RESULT 12
S00390

ig gamma chain (clone 36) - chicken (fragment)
N:Alternate names: Ig nu chain
C:Species: Gallus gallus (chicken)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000
C:Accession: S00390
R:Parvart, R.; Avizli, A.; Lentner, F.; Ziv, E.; Tel-Or, S.; Burstein, Y.; Schechter, R.
EMBO J. 7, 739-744, 1988
Article: Chicken immunoglobulin gamma-heavy chains: limited VH gene repertoire, combi
A:Reference number: S00390; MUID:88283642; PMID:3135182

F:436-455/Domain: carboxyl-terminal <CTS>
F:14/Disulfide bonds: Interchain (to light chain) #status predicted
F:28-89/Disulfide bonds: #status experimental
F:446-211,243:281,442/Binding site: carboxylate (Asp) (covalent) #status experimental
F:136-199,246-305,353-415/Disulfide bonds: #status predicted
F:218,434/Disulfide bonds: Interchain (to heavy chain) #status predicted
F:293/Disulfide bonds: Interchain (to mu chain in another subunit) #status predicted

Query Match 25.7% Score 439.5; DB 1; Length 455;
Best Local Similarity 32.3%; Pred. No. 2.7e-25;
Matches 106; Conservative 57; Mismatches 152; Indels 13; Gaps 8;

QY 4 PTVKILSSDCG-GGHFPPTIQLCLVSGYTPGTINITWLEDQVMDVLDSTASTTOEGE 62
DB 112 PNVNVEFVPRDGFSGPAPRKSCLKICEATNFTPKPTVSWLKDGLVESGFTTDPYTIENK 171
QY 63 LASTQ-----SELTLSQKHMLSDRTYTCQVYQGHF-EDSTKCADSNPRGVSAVLSRP 116
DB 172 GSTPQTYKVISTLTISEIDMLNLYTCRDVHRGLTFLKNVSSITCAASPTDILTFTIPR 231
QY 117 SPFDLFIKRSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHNSTRKEEKQRNGTLVFTSTL 176
DB 232 SFADIFLKSANLTCVNSNLATYE-TLNISWASQSGEPLETKIKIMESHNPMTFSAKGYA 290
QY 177 PVGTRDWIEGFTYOCRVTHPHLPALMRSTTKSGPRAAPEVYAFAP-EMPGSRDKRT 234
DB 291 SVCEEDMNNRKEFVCTVTHRDLPSPQKFKISKPNEVHKHPAVYLLPPAREQLNRESAT 350
QY 235 LACLIQNPREDISVQWLNHNEVQLPDARHSTTORPKTKGS-GF-FVFSRLEYTRAWEQK 292
DB 351 VTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPBEGAPGFYFTHSILTVTEEMNSG 410
QY 293 DEFICRAVHEAASPSQTVQRAVSNPGK 320
DB 411 ETYTCVGHGHAL-PHLYTERTVDKSTGK 437

RESULT 15

A24976
Ig mu chain C region (allele b) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
C:Accession: A24976
R:Schreier, P.H.; Quester, S.; Bothwell, A.
Nucleic Acids Res. 14, 2381-2389, 1986
A:Title: Allotypic differences in murine mu-genes
A:Reference number: A24976; MUID:86176735; PMID:3083402
A:Accession: A24976
A:Molecule type: mRNA
A:Residues: 1-455 <SCH>
A:Cross-references: GB:X03690; NID:952381; PIDN:CAA27326.1; PID:952382
A:Experimental source: strain C57BL/6
A>Note: the authors translated the codon AAG for residue 65 as Leu
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
C:Keywords: Immunoglobulin
F:346-417/Domain: Immunoglobulin homology <IMW>

Query Match 25.7% Score 439.5; DB 2; Length 455;
Best Local Similarity 32.3%; Pred. No. 2.7e-25;
Matches 106; Conservative 57; Mismatches 152; Indels 13; Gaps 8;

QY 4 PTVKILSSDCG-GGHFPPTIQLCLVSGYTPGTINITWLEDQVMDVLDSTASTTOEGE 62
DB 112 PNVNVEFVPRDGFSGPAPRKSCLKICEATNFTPKPTVSWLKDGLVESGFTTDPYTIENK 171
QY 63 LASTQ-----SELTLSQKHMLSDRTYTCQVYQGHF-EDSTKCADSNPRGVSAVLSRP 116
DB 172 GSTPQTYKVISTLTISEIDMLNLYTCRDVHRGLTFLKNVSSITCAASPTDILTFTIPR 231
QY 117 SPFDLFIKRSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHNSTRKEEKQRNGTLVFTSTL 176
DB 232 SFADIFLKSANLTCVNSNLATYE-TLNISWASQSGEPLETKIKIMESHNPMTFSAKGYA 290

QY 177 PVGTRDWIEGFTYOCRVTHPHLPALMRSTTKSGPRAAPEVYAFAP-EMPGSRDKRT 234
DB 291 SVCEEDMNNRKEFVCTVTHRDLPSPQKFKISKPNEVHKHPAVYLLPPAREQLNRESAT 350
QY 235 LACLIQNPREDISVQWLNHNEVQLPDARHSTTORPKTKGS-GF-FVFSRLEYTRAWEQK 292
DB 351 VTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPBEGAPGFYFTHSILTVTEEMNSG 410
QY 293 DEFICRAVHEAASPSQTVQRAVSNPGK 320
DB 411 ETYTCVGHGHAL-PHLYTERTVDKSTGK 437

Search completed: July 15, 2003, 06:59:32
Job time : 19.5549 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2003, 06:47:19 ; Search time 9.99108 Seconds
(without alignments)
1328.428 Million cell updates/sec

Title: US-09-847-208B-6

Perfect score: 1707

Sequence: 1 FTPTVRIKILSSCDGCHFP.....HEASPSQTVGRVSNPKG 320

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 1707 | 100.0 | 428 | 1 EPC_HUMAN | P01854 homo sapien |
| 2 | 793 | 46.5 | 429 | 1 EPC_RAT | P01855 rattus norv |
| 3 | 751 | 44.0 | 421 | 1 EPC_MOUSE | P06336 mus musculu |
| 4 | 439.5 | 25.7 | 455 | 1 MUC_MOUSE | P01872 mus musculu |
| 5 | 430.5 | 25.2 | 476 | 1 MUCM_MOUSE | P01873 mus musculu |
| 6 | 423.5 | 24.8 | 454 | 1 MUC_MESAU | P06337 mesocricetu |
| 7 | 416 | 24.4 | 326 | 1 GC2_HUMAN | P01859 homo sapien |
| 8 | 413.5 | 24.2 | 457 | 1 MUC_SUNMU | P20768 stuncus muri |
| 9 | 410 | 24.0 | 391 | 1 MUCB_HUMAN | P04220 homo sapien |
| 10 | 405.5 | 23.8 | 454 | 1 MUC_HUMAN | P01871 homo sapien |
| 11 | 405.5 | 23.8 | 458 | 1 MUC_RABIT | P03988 coryctolagus |
| 12 | 404.5 | 23.7 | 329 | 1 GC2_CAVPO | P01862 cavia porce |
| 13 | 402 | 23.6 | 324 | 1 GC1_MOUSE | P01868 mus musculu |
| 14 | 399 | 23.4 | 330 | 1 GCMA_MOUSE | P01863 mus musculu |
| 15 | 397.5 | 23.3 | 330 | 1 GC1_HUMAN | P01857 homo sapien |
| 16 | 397 | 23.3 | 333 | 1 GC1M_MOUSE | P01869 mus musculu |
| 17 | 396.5 | 23.2 | 479 | 1 MUCM_RABIT | P04221 coryctolagus |
| 18 | 394 | 23.1 | 399 | 1 GCAM_MOUSE | P01865 mus musculu |
| 19 | 390 | 22.8 | 336 | 1 GCB_MOUSE | P01866 mus musculu |
| 20 | 389 | 22.8 | 450 | 1 MOC_CANFA | P01874 canis famli |
| 21 | 386.5 | 22.6 | 323 | 1 GC_RABIT | P01870 coryctolagus |
| 22 | 386.5 | 22.6 | 329 | 1 GGC_RAT | P20762 rattus norv |
| 23 | 385.5 | 22.6 | 327 | 1 GC4_HUMAN | P01861 homo sapien |
| 24 | 385.5 | 22.6 | 333 | 1 GCB_RAT | P20761 rattus norv |
| 25 | 385 | 22.6 | 405 | 1 GCBM_MOUSE | P01867 mus musculu |
| 26 | 377 | 22.1 | 329 | 1 GCS_MOUSE | P22436 mus musculu |
| 27 | 376 | 22.0 | 322 | 1 GCA_RAT | P20760 rattus norv |
| 28 | 369 | 21.6 | 326 | 1 GC1_RAT | P20759 rattus norv |
| 29 | 366 | 21.4 | 398 | 1 GC3M_MOUSE | P03987 mus musculu |
| 30 | 362.5 | 21.2 | 335 | 1 GCAB_MOUSE | P01864 mus musculu |
| 31 | 347 | 20.3 | 340 | 1 ALG2_HUMAN | P01877 homo sapien |
| 32 | 345.5 | 20.2 | 290 | 1 GC3_HUMAN | P01860 homo sapien |
| 33 | 334.5 | 19.6 | 353 | 1 ALG1_HUMAN | P01876 homo sapien |

| | | | | | |
|----|-------|------|-----|--------------|---------------------|
| 34 | 327 | 19.2 | 438 | 1 HVCS_HETFR | P23087 heterodontu |
| 35 | 326 | 19.1 | 353 | 1 ALG1_GORGO | P20758 gorilla gor |
| 36 | 324 | 19.0 | 438 | 1 HVG2_HETFR | P23085 heterodontu |
| 37 | 321 | 18.8 | 393 | 1 HVG3_HETFR | P23086 heterodontu |
| 38 | 318 | 18.6 | 461 | 1 HVCM_HETFR | P23088 heterodontu |
| 39 | 310 | 18.2 | 446 | 1 MOC_CHICK | P01875 gallus gall |
| 40 | 304 | 17.8 | 370 | 1 HVG1_HETFR | P23084 heterodontu |
| 41 | 303 | 17.8 | 344 | 1 ALC_MOUSE | P01878 mus musculu |
| 42 | 236.5 | 13.9 | 299 | 1 ALC_RABIT | P01879 coryctolagus |
| 43 | 228.5 | 13.4 | 481 | 1 MUCM_ICTPU | P23735 ictalurus p |
| 44 | 193 | 11.3 | 383 | 1 DTC_HUMAN | P01880 homo sapien |
| 45 | 148 | 8.7 | 104 | 1 LAC2_RAT | P20767 rattus norv |

ALIGNMENTS

| RESULT 1 | ID | EPIC_HUMAN | STANDARD; | PRT; | 428 AA. |
|----------|--|------------|-----------|------|---------|
| AC | P01854: | | | | |
| DT | 21-JUL-1986 (rel. 01, Created) | | | | |
| DT | 21-JUL-1986 (rel. 01, Last sequence update) | | | | |
| DT | 15-JUN-2002 (rel. 41, Last annotation update) | | | | |
| DE | Ig epsilon chain C region. | | | | |
| GN | IGH. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=83168897; PubMed=6300763; | | | | |
| RA | Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K., | | | | |
| RA | Kikuchi M., Sugino Y., Nishida Y., Honjo T.; | | | | |
| RT | "Molecular cloning and nucleotide sequencing of human immunoglobulin | | | | |
| RT | epsilon chain cDNA." | | | | |
| RL | Nucleic Acids Res. 11:719-726(1983). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A., AND VARIANT LEU-359. | | | | |
| RX | MEDLINE=83001945; PubMed=6288268; | | | | |
| RA | Max E.E., Batley J., Ney R., Kirsch I.R., Leder P.; | | | | |
| RA | "The sequence of a human immunoglobulin epsilon chain constant | | | | |
| RT | region gene, and evidence for three non-allelic genes." | | | | |
| RL | EMBO J. 1:655-660(1982). | | | | |
| RN | [3] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=84236029; PubMed=6234164; | | | | |
| RA | Flanagan J.G., Rabbits T.H.; | | | | |
| RT | "The sequence of a human immunoglobulin epsilon chain constant | | | | |
| RT | region gene, and evidence for three non-allelic genes." | | | | |
| RL | EMBO J. 1:655-660(1982). | | | | |
| RN | [4] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=84207910; PubMed=6327276; | | | | |
| RA | Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.; | | | | |
| RT | "Long terminal repeat-like elements flank a human immunoglobulin | | | | |
| RT | epsilon pseudogene that lacks introns." | | | | |
| RL | EMBO J. 1:1539-1544(1982). | | | | |
| RN | [5] | | | | |
| RP | PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND). | | | | |
| RA | Benlich H.H., Johansson S.G.O., von Bahr-Lindstrom H.; | | | | |
| RT | (In) Bach M.K. (eds.); | | | | |
| RL | Immediate hypersensitivity: modern concepts and developments, pp.1-36, | | | | |
| RL | Marcel Dekker, New York (1978). | | | | |
| RN | [6] | | | | |
| RP | SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A. | | | | |
| RX | MEDLINE=83065234; PubMed=6815656; | | | | |
| RA | Kentzen J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J., | | | | |
| RA | Bell L.O., Gould H.J.; | | | | |
| RT | "Cloning and sequence determination of the gene for the human | | | | |
| RT | immunoglobulin epsilon chain expressed in a myeloma cell line." | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982). | | | | |
| RN | [7] | | | | |

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RP 3D-STRUCTURE MODELING.
RX MEDLINE=87089848; PubMed=3796618;
RA Padlan E.A.; Davies D.R.;
RT "A model of the Fc of immunoglobulin E.";
RL Mol. Immunol. 23:1053-1075(1986).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L00022; AAB59424.1; ALT_INIT.
DR PIR: A02142; EHHT.
DR PIR: A22771; A22771.
DR PIR: A23195; A23195.
DR PDB: 1IGE; 15-JUL-92.
DR Genew: HGNC:5522; IGHE.
DR MIM: 147180; .
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003597; IG_c1.
DR Pfam: PF00047; 1g; 4.
DR SMART: SM00407; IGc1; 4.
DR PROSITE: PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW 3D-structure.
FT NOY TER 1 1
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 15 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 29 85 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 121 121 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 135 193 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 209 209 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 239 299 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 345 405 INTERCHAIN (WITH A HEAVY CHAIN).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .).
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .).
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .).
FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .).
FT VARIANT 359 359 W -> L (POSSIBLE POLYMORPHISM).
FT /FTID=VAR.003885.
SQ SEQUENCE 428 AA; 47019 MW; 25C4CA072AA558A0 CRC64;
Query Match 100.0%; Score 1707; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.7e-129;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FTPTVILIOSSCGGHPPTIOLCLVSGYPTGTINIMWLEDGOVMDVLDLSTASTOE 60
DB 109 FTPTVILIOSSCGGHPPTIOLCLVSGYPTGTINIMWLEDGOVMDVLDLSTASTOE 168
OY 61 GELASTOSELTLSOKHMLSDRTYTCQVYTGHTFEDSTKCADSNPGRVSAVLSRPSFD 120
DB 169 GELASTOSELTLSOKHMLSDRTYTCQVYTGHTFEDSTKCADSNPGRVSAVLSRPSFD 228
OY 121 LFIKSTTICLVVDLAPSKGYVLTWSRASGKRVNHSRKEKORNGTGLTVSTLPVGT 180
DB 229 LFIKSTTICLVVDLAPSKGYVLTWSRASGKRVNHSRKEKORNGTGLTVSTLPVGT 288
OY 181 RDMIEGTYOCRTVTHPLPRALMRSTKTSGRAPRVYAFAPPEWGSFDRKTLALIO 240
DB 289 RDMIEGTYOCRTVTHPLPRALMRSTKTSGRAPRVYAFAPPEWGSFDRKTLALIO 348
OY 241 NFMPEDISVOMLNEVOLDPARHSTTOPRKTKSGGFVFSRLLEYTRAEMEKDEFICRAV 300
DB 349 NFMPEDISVOMLNEVOLDPARHSTTOPRKTKSGGFVFSRLLEYTRAEMEKDEFICRAV 408
OY 301 HEAASPSQTVQRAVSNPCK 320
IIIIIIIIIIIIIIIIIIIIII

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DB 409 HEAASPSQTVQRAVSNPCK 428
RESULT 2
ID EPC_RAT STANDARD: PRT: 429 AA.
AC P01855;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig epsilon chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).
RC STRAIN=LOU/C/MSL;
RX MEDLINE=83064537; PubMed=6292865;
RA Hellman L., Pettersson U., Engstrom A., Karlsson T., Bennich H.;
RT "Structure and evolution of the heavy chain from rat immunoglobulin
RT E.".
RL Nucleic Acids Res. 10:6041-6049(1982).
RN (2)
RP SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
RX MEDLINE=83182019; PubMed=6820340;
RA Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
RT "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:
RT construction, identification, and DNA sequence.";
RL DNA 1:335-343(1982).
RN (3)
RP SEQUENCE OF 205-306 FROM N.A.
RX MEDLINE=82174576; PubMed=6803238;
RA Hellman L., Pettersson U., Bennich H.;
RT "Characterization and molecular cloning of the mRNA for the heavy
RT (epsilon) chain of rat immunoglobulin E.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
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CC -----
DR EMBL: J00744; AAA41379.1; ALT_INIT.
DR PIR: A02143; EHRT.
DR HSSP: P01854; 1IGE.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003597; IG_c1.
DR InterPro: IPR003600; IG_Like.
DR Pfam: PF00047; 1g; 4.
DR SMART: SM00410; IG_Like; 3.
DR SMART: SM00407; IGc1; 1.
DR PROSITE: PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NOY TER 1 1
FT CONFLICT 168 168 R -> N (IN REF. 2).
FT CONFLICT 308 308 P -> L (IN REF. 2).
SQ SEQUENCE 429 AA; 48671 MW; D2970B34EF8A72B0 CRC64;
Query Match 46.5%; Score 793; DB 1; Length 429;
Best Local Similarity 47.4%; Pred. No. 3.4e-56;
Matches 152; Conservative 54; Mismatches 109; Indels 6; Gaps 5;
OY 2 TPTVILIOSSCGGHPPTIOLCLVSGYPTGTINIMWLEDGOVMDVLDLSTASTOE 60
DB 101 TPTVILIOSSCGGHPPTIOLCLVSGYPTGTINIMWLEDGOVMDVLDLSTASTOE 159
OY 61 GELASTOSELTLSOKHMLSDRTYTCQVYTGHTFEDSTKCADSNPGRVSAVLSRPSFD 120
DB 160 GELASTOSELTLSOKHMLSDRTYTCQVYTGHTFEDSTKCADSNPGRVSAVLSRPSFD 219

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QY 121 LFIKSPITCLVVDLPASRGVNLWLSRASGKPVNHSSTREKORNGTLVTSILPVG 180
D 220 LVENGTFKRLICLVLDL-ESEENITVTVWRERKKSIGASQSTKHNNATISITSLPVDA 278
QY 181 KDWIEGTYOGRVTHPHLPRLALMRSTKTSGRPARAPVYVAFAPDEWPGSRDKRTLACLIQ 240
D 279 KDWIEGTYOGRVTHPHLPRLALMRSTKTSGRPARAPVYVAFAPDEWPGSRDKRTLACLIQ 337
QY 241 NFMEDISVQMLNHEVOLPDARHSTTOPRKTGSG--FFVYSRLLEVTRAEMEQDEFICR 298
D 338 NFMEDISVQMLNHEVOLPDARHSTTOPRKTGSG--FFVYSRLLEVTRAEMEQDEFICR 397
QY 299 AVHEASPSQTVQRAVSNPG 319
D 398 VIHEALQPKRLKERTISLIG 418

RESULT 3
EPC_MOUSE STANDARD; PRT; 421 AA.
ID EPC_MOUSE STANDARD; PRT; 421 AA.
AC P06336; P01856; (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig epsilon chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84236092; PubMed=6329728;
RA Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
RT "The nucleotide sequence of the mouse immunoglobulin epsilon gene:
RL comparison with the human epsilon gene sequence."
RN [2]
RP REVISIONS.
RA Honjo T.;
RL Submitted (APR-1986) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 34-421 FROM N.A.
RX MEDLINE=83117774; PubMed=6818553;
RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
RT "Cloning and nucleotide sequence of mouse immunoglobulin epsilon
RL chain cDNA."
RL Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
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CC -----
DR EMBL: X01857; CAA25977.1; -
DR EMBL: X01857; CAA25978.1; -
DR PIR: A02145; EHMS.
DR PIR: A02144; EHMS.
DR HSSP: P01854; IIGF.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003597; IG_C1.
DR InterPro: IPR003600; IG_Like.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00410; IG_Like; 2.
DR SMART: SM00407; IG_C1; 2.
DR PROSITE: PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 90 CH1.
FT DOMAIN 91 197 CH2.

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FT DOMAIN 198 304 CH3.
FT DOMAIN 305 421 CH4.
FT DISULFID 23 75 BY SIMILARITY.
FT DISULFID 121 180 BY SIMILARITY.
FT DISULFID 226 285 BY SIMILARITY.
FT DISULFID 330 392 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 421 AA; 47320 MW; 8F909E130A06B47 CRC64;

Query Match 44.0%; Score 751; DB 1; Length 421;
Best Local Similarity 45.8%; Pred. No. 7.5e-53;
Matches 147; Conservative 59; Mismatches 109; Indels 6; Gaps 5;

QY 2 TPPTVKILQSSCDGGHFRPTIOLCLVSGTPTGINTWL-EDGYMDVDLSTASTOE 60
D 97 TEPTLELHSSCDPNA-FHSTIOLCEFTYGHILNDVSVWMLDDREITDVLQVLIKEE 155
QY 61 GELASTQSELTLISQKHWLSDRTYQVYOGHFTEDSTKRCADSNPRGVSATLSRPSF 120
D 156 GKLASTQSKLNTITQOMMSEETFTCKYTSQGVLDLHTRCRDHPERGVIYLLRPSPLD 215
QY 121 LFIKSPITCLVVDLPASRGVNLWLSRASGKPVNHSSTREKORNGTLVTSILPVG 180
D 216 LYQNGAPKRLICLVLDLSEK-NVNVTNQOEKTSVASQWYTKHNNATISITSLPVDA 274
QY 181 KDWIEGTYOGRVTHPHLPRLALMRSTKTSGRPARAPVYVAFAPDEWPGSRDKRTLACLIQ 240
D 275 KDWIEGTYOGRVTHPHLPRLALMRSTKTSGRPARAPVYVAFAPDEWPGSRDKRTLACLIQ 333
QY 241 NFMEDISVQMLNHEVOLPDARHSTTOPRKTGSG--FFVYSRLLEVTRAEMEQDEFICR 298
D 334 NFMEDISVQMLNHEVOLPDARHSTTOPRKTGSG--FFVYSRLLEVTRAEMEQDEFICR 397
QY 299 AVHEASPSQTVQRAVSNPG 319
D 394 VIHEALQPKRLKERTISLIG 414

RESULT 4
MOC_MOUSE STANDARD; PRT; 455 AA.
ID MOC_MOUSE STANDARD; PRT; 455 AA.
AC P01872;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig mu chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076590; PubMed=6255422;
RA Kawakami T., Takahashi N., Honjo T.;
RT "Complete nucleotide sequence of mouse immunoglobulin mu gene and
RL comparison with other immunoglobulin heavy chain genes."
RN [2]
RP Nucleic Acids Res. 8:3933-3945(1980).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=82051295; PubMed=6795090;
RA Goldberg G.I., Vanin E.F., Zrolka A.M., Blattner F.R.;
RT "Sequence of the gene for the constant region of the mu chain of
RL Balb/c mouse immunoglobulin."
RN [3]

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| Query Match | Score | DB 1 | Length |
|---|-------|------|--------|
| RP SEQUENCE FROM N.A. (MYELOMA TEPC183). | 455 | AA | 50101 |
| RX MEDLINE-81165562; Pubmed-6260591; | 455 | AA | 50101 |
| RA Aufray C., Rougeon F.; | 455 | AA | 50101 |
| RT "Nucleotide sequence of a cloned cDNA corresponding to secreted mu chain of mouse immunoglobulin."; | 455 | AA | 50101 |
| RL Gene 12:77-86(1980). | 455 | AA | 50101 |
| RN [4] | 455 | AA | 50101 |
| RP SEQUENCE (MYELOMA PROTEIN MOPC 104E). | 455 | AA | 50101 |
| RX MEDLINE-79223904; Pubmed-111247; | 455 | AA | 50101 |
| RA Kelly M.R., Sibley C.H., Fuhrman J.S., Schilling J.W., Hood L.E.; | 455 | AA | 50101 |
| RT "Amino acid sequence of a mouse immunoglobulin mu chain."; | 455 | AA | 50101 |
| RL Proc. Natl. Acad. Sci. U.S.A. 76:2932-2936(1979). | 455 | AA | 50101 |
| RN [5] | 455 | AA | 50101 |
| RP REVISION (MOPC 104E). | 455 | AA | 50101 |
| RX MEDLINE-83075344; Pubmed-6816276; | 455 | AA | 50101 |
| RA Kelly M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H., Hood L.E.; | 455 | AA | 50101 |
| RT "Complete amino acid sequence of a mouse mu chain: homology among heavy chain constant region domains."; | 455 | AA | 50101 |
| RL Biochemistry 21:5415-5424(1982). | 455 | AA | 50101 |
| CC -I- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCYTES SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF IGM. THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C-TERMINAL SEGMENTS. | 455 | AA | 50101 |
| CC ----- | 455 | AA | 50101 |
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| CC ----- | 455 | AA | 50101 |
| DR EMBL; V00827; -; NOT_ANNOTATED_CDS. | 455 | AA | 50101 |
| DR PIR; A02166; MEMS. | 455 | AA | 50101 |
| DR HSSP; P01857; 1PCL. | 455 | AA | 50101 |
| DR InterPro: IPR003106; Ig_MHC. | 455 | AA | 50101 |
| DR InterPro: IPR003597; Ig_C1. | 455 | AA | 50101 |
| DR InterPro: IPR003600; Ig_Like. | 455 | AA | 50101 |
| DR Pfam; PF00047; Ig; 4. | 455 | AA | 50101 |
| DR SMART; SM00410; Ig_Like; 2. | 455 | AA | 50101 |
| DR SMART; SM00410; IgC1; 2. | 455 | AA | 50101 |
| DR PROSITE; PS00290; IG_MHC; 3. | 455 | AA | 50101 |
| KM Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; | 455 | AA | 50101 |
| KW Alternative splicing. | 455 | AA | 50101 |
| FT NON_TER 1 | 455 | AA | 50101 |
| FT DOMAIN 1 105 | 455 | AA | 50101 |
| FT DOMAIN 106 217 | 455 | AA | 50101 |
| FT DOMAIN 218 324 | 455 | AA | 50101 |
| FT DOMAIN 325 436 | 455 | AA | 50101 |
| FT DOMAIN 437 455 | 455 | AA | 50101 |
| FT DISULFID 14 14 | 455 | AA | 50101 |
| FT DISULFID 28 89 | 455 | AA | 50101 |
| FT DISULFID 136 199 | 455 | AA | 50101 |
| FT DISULFID 216 216 | 455 | AA | 50101 |
| FT DISULFID 246 305 | 455 | AA | 50101 |
| FT DISULFID 293 293 | 455 | AA | 50101 |
| FT DISULFID 353 415 | 455 | AA | 50101 |
| FT DISULFID 454 454 | 455 | AA | 50101 |
| FT CARBOHYD 46 46 | 455 | AA | 50101 |
| FT CARBOHYD 211 211 | 455 | AA | 50101 |
| FT CARBOHYD 243 243 | 455 | AA | 50101 |
| FT CARBOHYD 281 281 | 455 | AA | 50101 |
| FT CARBOHYD 442 442 | 455 | AA | 50101 |
| FT VARIANT 78 78 | 455 | AA | 50101 |
| FT VARIANT 101 101 | 455 | AA | 50101 |
| FT VARIANT 226 226 | 455 | AA | 50101 |
| FT VARIANT 258 258 | 455 | AA | 50101 |
| FT VARIANT 258 258 | 455 | AA | 50101 |
| FT VARIANT 368 368 | 455 | AA | 50101 |
| SS SEQUENCE 455 AA; 50101 MM; 4CB5E7C6B02F9B51 CRC64; | 455 | AA | 50101 |

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Best LocalSimilarity 32.3%, Pred. No.6-7e-28; Mismatches 106; Conservative .57; Mismatches 152; Indels 13; Gaps 8;
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| | | | | |
|----|--|-----|--|-----|
| OY | | 4 | PVKKILOSSCDG-GGHPPPTQLCLVSGVPRTINITWLEDGOVMVDLSTASTQOGE | 62 |
| Dd | | 112 | PNVNVEFVRPRGFSGPAPRASKKLICEATNFMPKPIIVASWLMDGLVSEGFTDPEVTENK | 171 |
| OY | | 63 | LASNQ-----SELTSLOKHMLSDRYTTCOVLYOGHTF-EDSTKKCADSNPGVASYLSPR | 116 |
| Dd | | 172 | GSIPTTYKVISTISIELDMNLNVYTICRVHRGLTFELKNVSIFCAASPSSDIILFTIP | 231 |
| OY | | 117 | SFFDLFIKRSPTITC LVLDLPASRGYNVLTVMSRASGRKEVNSTRKEEQRNGTLITVSTL | 176 |
| Dd | | 232 | SFADFLEFSKANLCIAVNSLATYE-TLNISWASOSGEPLFKIKIMESHPNGTESAKOVA | 290 |
| OY | | 177 | PVGTRDWIEGETYOQCRTYHPHLPRLAMSTKTGSRAAPEVYAFTP--EMPSRDRT | 234 |
| Dd | | 291 | SVCEEDMNRRNEFECTVTHROLJPSPOCKEFISKPREVHKHPAVUYLLPARBOLNRESAT | 350 |
| OY | | 235 | IACLIQNPMPEDISQMVLHNENVQLRPDAHSITYOPRKTKGS-G-FVFSLREVTARAEMPOK | 292 |
| Dd | | 351 | VTCLVKGSRPADISVOMLRQROQLRPOEKYYYSARMPREGAGCFYTHSILTIVEENNIG | 410 |
| OY | | 293 | DEFICRAYHEAASSQTVOARAYSNPCPK | 320 |
| Dd | | 411 | EYTCVVGGHEAL-PHLVTERFDVKSTGK | 437 |

RESULT 5
MCM_MOUSE ID MCM_MOUSE STANDARD PRG 476 AA.

| | | |
|-----|---|--------------------------------|
| AC | P01873: | 21-JUL-1986 (Rel. 01, Created) |
| DT | 01-NOV-1991 (Rel. 20, Last sequence update) | |
| DE | 15-JUL-1999 (Rel. 38, Last annotation update) | |
| ID | Ig mu chain C region membrane-bound form. | |
| MUS | musculus (Mouse). | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| OX | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | |
| NBI | TaxID=10090; | (1) |
| RN | SEQUENCE OF 433-476 FROM N.A. | |
| RX | MEDLINE=8022874; PubMed=6771020; | |
| RA | Hood L.; Rogers J., Davis M., Calame K., Bond M., Wall R, | |
| RT | "Two mRNAs can be produced from a single immunoglobulin mu gene by alternative RNA processing pathways." | [1] |
| RL | Cell 20:313-319(1980). [2] | |
| RP | SEQUENCE OF 410-476 FROM N.A. (MYELOMA MOPC 104E). | |
| RX | MEDLINE=8022873; Pubmed=6771019; | |
| RA | Rogers J., Early P., Carter C., Calame K., Bond W., Hood L, | |
| RT | Wall R; | |
| RL | "Two mRNAs with different 3' ends encode membrane-bound and secreted forms of immunoglobulin mu chain."; | |
| CC | -!- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCYTES SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF IGM. THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C- | |
| CC | TERMINAL SEGMENTS. | |
| CC | -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-409 IS ASSUMED TO BE IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM. | |
| CC | ---- | |
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| OR | EMBL; V00821.CAA24202.1; - | |
| OR | PIR; A02167; MHSM. | |

DR HSPD; P01857; 1fcl.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig-cl.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig_4.
 DR SMART; SM00410; Ig_Like; 2.
 DR SMART; SM00407; Igc1; 2.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing; Transmembrane.
 FT NON_TER 1
 FT DOMAIN 1 105 CH1.
 FT DOMAIN 106 217 CH2.
 FT DOMAIN 218 324 CH3.
 FT DOMAIN 325 436 CH4.
 FT TRANSMEM 456 473 POTENTIAL.
 FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
 FT DISULFID 28 89
 FT DISULFID 136 199 BY SIMILARITY.
 FT DISULFID 136 199 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 FT DISULFID 246 305 BY SIMILARITY.
 FT DISULFID 293 293 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 FT DISULFID 353 415 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .).
 SQ SEQUENCE 476 AA; 52656 MW; 80476575A5204071 CRC64;

Query Match 25.2%; Score 430.5; DB 1; Length 476;
 Best Local Similarity 32.3%; Pred. No. 3.7e-27;
 Matches 104; Conservative 56; Mismatches 149; Indels 13; Gaps 8;

QY 4 PTVKLISSCGG-GGHPPTIOLCLVSGYPTGNTINIMLEGGQVMDVLDLSTASTQGE 62
 DB 112 PNVAVFVPSRDAFSGPAPKRSRLFCFASNFSEKQITVSLRGDKPVKSGFTTPTPDR 171
 QY 63 LASTO-----SELTLSOKHMLSDRTYTCOVYQGHF-EDSKKCADSNPRGVAYLSRP 116
 DB 172 GSTPQTYKVIISLTITSELDMLNLYTCRVDRHGLTFKKNVSTCAASSTIOAFPIRP 231
 QY 117 SPFDLFIKSPPTITLVVDLAPSKGTNLMTWSRASKPVNHSRREKORNGTLTVSTL 176
 DB 232 SFADIFFLKSANLTLVSNLAHYE-TLNIISMAOSGEPLFTKIKIMESHNPNGTFSAGVA 290
 QY 177 PVTGDMWIGETVOCRVTHPHLPRALMRSTTKTSGPRAPVYATP--EMPGSRDKRT 234
 DB 291 SYCVEDMNNKKEFVCTVTHRDLPSPQKFKISKPNVHKHPVAYLLPPAREQLNRESAT 350
 QY 235 IACLIONFMPEDISVQMLHNEVOLDPARHSTTOPRKTGS-GF-FVFSRLLEYTRAWECK 292
 DB 351 VTCLVKGFSPADISVQMLQROGLPQEKYVTSAPMPREQAPRFYTHSLITYTEEMNGC 410
 QY 293 DEFICRAVHEAASPSQTVORAV 314
 DB 411 EYTCVGVGHEAL-PHLYTERTV 431

RESULT 6
 MUC_MESAU
 ID MUC_MESAU STANDARD; PRT; 454 AA.
 AC P06337;
 DT 01-JAN-1988 (rel. 06, Created)
 DT 01-FEB-1996 (rel. 33, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE Ig mu chain C region.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_Taxid=10036;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=85297761; PubMed=2994005;
 RA McGuire K.L., Duncan W.R., Tucker P.W.;
 RT "Phylogenetic conservation of immunoglobulin heavy chains: direct
 RT comparison of hamster and mouse Cmu genes".
 RL Nucleic Acids Res. 13:5611-5628(1985).
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; X02804; CAA26574.1; -
 DR PIR; A02168; MHVY.
 DR HSPD; P01854; 1fcl.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig-cl.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig_4.
 DR SMART; SM00410; Ig_Like; 2.
 DR SMART; SM00407; Igc1; 2.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 KW NON_TER 1
 KW DOMAIN 1 105 CH1.
 KW DOMAIN 106 218 CH2.
 KW DOMAIN 219 324 CH3.
 KW DOMAIN 325 454 CH4.
 KW DISULFID 13 13 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
 KW DISULFID 27 88 BY SIMILARITY.
 KW DISULFID 135 198 BY SIMILARITY.
 KW DISULFID 215 215 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 KW DISULFID 245 304 BY SIMILARITY.
 KW DISULFID 292 292 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 KW DISULFID 352 414 BY SIMILARITY.
 KW DISULFID 453 453 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 KW CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
 KW CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
 KW CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
 KW CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
 KW CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 KW CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
 KW CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
 KW CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 454 AA; 50196 MW; 4DA2134612BE1469 CRC64;

Query Match 24.8%; Score 423.5; DB 1; Length 454;
 Best Local Similarity 31.5%; Pred. No. 1.3e-26;
 Matches 106; Conservative 56; Mismatches 145; Indels 29; Gaps 10;

QY 4 PTVKLISSCGG-GGHPPTIOLCLVSGYPTGNTINIMLEGGQVMDVLDLSTASTQGE 62
 DB 111 PNVAVFVPSRDAFSGPAPKRSRLFCFASNFSEKQITVSLRGDKPVKSGFTTPTPDR 170
 QY 63 LASTO-----SELTLSOKHMLSDRTYTCOVYQGHF-EDSKKCADSNPRGVAYLSRP 116
 DB 171 GSGPRTYKVIISLTITSELDMLNLYTCRVDRHGLTFKKNVSTCAASSTIOAFPIRP 230
 QY 117 SPFDLFIKSPPTITLVVDLAPSKGTNLMTWSRASKPVNHSRREKORNGTLTVSTL 176
 DB 231 SFVGIFLKSANLTLVSNLA-TYPLNIISSSRSGEPLFTKIKIMESHNPNGTFSAGBA 289
 QY 177 PVTGDMWIGETVOCRVTHPHLPRALMRSTTKTSGPR-----AAPEYVATPTEWGSRDK 232
 DB 290 NVCVEDMWSGKEFVCTVTHRDLPSPQKFKISK--PREMNKTPVAVY-----QDPLARQ 341
 QY 233 -----RTACLIONFMPEDISVQMLHNEVOLDPARHSTTOPRKTGS--FVFSRLLEV 284
 DB 342 LILRESATVTCVKGFSPADISVQMLQROGLPQEKYVTSAPMPREQAPRHLYFTSVLTV 401
 QY 285 TRAEWQKDEFICRAVHEAASPSQTVORAVSNPK 320

Db 402 TEEMNGSEYTCVGHDL-PHNVETKDRSTGK 436

RESULT 7

GC2_HUMAN STANDARD: PRT: 326 AA.

AC P01859; 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Ig gamma-2 chain C region.

GN IGHG2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_Taxid:9606;

RP [1]

RP SEQUENCE OF 2-326 FROM N.A.

RX MEDLINE-82197621; PubMed-6804948;

RA Ellison J.W., Hood L.E.;

RT "Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes.";

RT Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).

RL [2]

RP SEQUENCE OF 88-115 FROM N.A.

RC TISSUE-Fetal liver;

RX MEDLINE-83001943; PubMed-6811139;

RA Takahashi N., Ueda S., Obata M., Nakai S., Honjo T.;

RT "Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";

RT Cell 29:671-679(1982).

RL [3]

RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.

RC TISSUE-Fetal liver;

RX MEDLINE-8423592; PubMed-6329676;

RA Krawinkel U., Rabbits T.H.;

RT "Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes.";

RT EMBO J. 1:403-407(1982).

RL [4]

RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).

RX MEDLINE-81007873; PubMed-6774012.

RA Wang A.-C., Tung E., Fudenberg H.H.;

RT "The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.";

RT J. Immunol. 125:1048-1054(1980).

RL [5]

RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).

RX MEDLINE-80001357; PubMed-113080;

RA Connell G.E., Parr D.M., Hofmann T.;

RT "The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";

RT Can. J. Biochem. 57:758-767(1979).

RL [6]

RP SEQUENCE OF 238-275 (ZIE).

RX MEDLINE-80114419; PubMed-118920;

RA Hofmann T., Parr D.M.;

RT "A note of the amino acid sequence of residues 381-391 of human immunoglobulin gamma chains.";

RT Mol. Immunol. 16:923-925(1979).

RL [7]

RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).

RA Hofmann T., Parr D.M.;

RL Submitted (MAR-1980) to the PIR data bank.

RP [8]

RP SEQUENCE OF 1-121 (DOR).

RX MEDLINE-95255296; PubMed-7737190;

RA Scoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;

RT "Characterization of the two unique human anti-flavin monoclonal immunoglobulins.";

RT Eur. J. Biochem. 228:886-893(1995).

RM [9]

RP DISULFIDE BONDS.

RX MEDLINE-72033500; PubMed-4940472;

RA Milstein C., Frangione B.;

RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";

RL Biochem. J. 121:217-225(1971).

RM [10]

RP DISULFIDE BONDS.

RX MEDLINE-69064124; PubMed-5782707;

RA Frangione B., Milstein C., Plink J.R.L.;

RT "Structural studies of immunoglobulin G.";

RL Nature 221:145-148(1969).

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CC EMBL: J00230; AAB59393.1; -

DR PIR: A02148; G2HU.

DR HSSP: P01857; IRL1.

DR Genew: HGNC:5526; IGHG2.

DR MIM: 147110; -

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003597; Ig_c1.

DR InterPro: IPR003600; Ig_Like.

DR Pfam: PF00047; Ig_3.

DR SMART: SM00410; Ig_Like; 1.

DR SMART: SM00407; Ig_c1; 2.

DR PROSITE: PS00290; Ig_MHC; 2.

DR Immunoglobulin domain; Immunoglobulin C region.

FW NON_TER 1 1

FT DOMAIN 1 98 CH1.

FT DOMAIN 99 110 HINGE.

FT DOMAIN 111 219 CH2.

FT DOMAIN 220 326 CH3.

FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 140 200 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 246 304

FT SITE 156 156

FT MOD_RES 326 326

FT VARIANT 60 60

FT CONFLICT 109 109

FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;

SO

Query Match 24.4%; Score 416; DB 1; Length 326;

Best Local Similarity 31.28; Pred. No. 3,4e-26;

Matches 105; Conservative 59; Mismatches 136; Indels 36; Gaps 11;

QY 11 SSCDGGGHP-----PTIQLCLVAGYPTGNTIWEDEGVADVLDLSTASTQ 60

DB 1 ASKRGSPVFPPLACRSSTSESTALGCLVADYDFPEPTVSM-NSGALTSGVHFPAYLOS 59

QY 61 GELASTQSELTLSOKHMLSDRTYTCQVYQ-NGHTEEDST--KKCADSNP-----RGVS 110

DB 60 SGLYSLSSVTVPSNSF-GTQYTCVNDHDKPSNKTVERKCCVCPCPAPVPVAGPS 118

QY 111 AYLSRSPSPD-LPIKSPITITCLVVDLAPSKGYNLWTSASGKPVVHSTRKEKQRNGT 169

DB 119 VFLEPPRPKDTLMSIRPPEVTCVVDVSHDPEQFMWYDVGEVHNAAKTRPREDFNST 178

QY 170 LVTSTLPVGTWRMIESETYQCRTHPHLPRALMRSTKSGPAAEVYAFATPEWPGS 229

DB 179 FRVVSUTLVVHODMLNKEKCKVSNKGLPALEKTIKTKGQPREQVITL-----PPS 233

QY 230 RDKRT-----LACLIQNFMEPDISVQWLHNEVOLPDARHSTTOPRKTKSGFVEFSRLEV 284
 Db 234 REENTKNQVSLTCLVKEFYPSDLAVENSN--GGPENNYKTTTPMDSDSFLYSLTY 291
 QY 285 TRAEWECKDEFFICRAVHEAASPSQTVORAVSVNPGK 320
 Db 292 DKSRMOGNAVFCSSVMHEALHNHYT--OKSLSLSPGK 326

RESULT 8
 MOCB_HUMAN
 ID MOCB_SUNMU STANDARD; PRT; 457 AA.
 AC P20768;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 1g mu chain C region.
 OS Suncus murinus (House shrew) (Musk shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Soricidae; Crocidurinae; Suncus.
 NCBI_TaxID=9378;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=69232144; PubMed=2497033;
 RA Ishiguro H., Ichihara Y., Namikawa T., Nagatsu T., Kurosawa Y.;
 RT "Nucleotide sequence of Suncus murinus immunoglobulin mu gene and
 RL comparison with mouse and human mu genes.";
 FEBS Lett. 247:317-322(1989).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X13920; CAA32113.1; ALT_INT.
 DR PTR: S03961; S03961.
 DR HSSP: P01842; 7FAB.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003600; Ig_like.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00410; Ig_like; 1.
 DR SMART: SM00407; Igcl; 3.
 DR PROSITE: PS00290; Ig_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region; glycoprotein.
 FT NON_TER 1 105 CH1.
 FT DOMAIN 106 220 CH2.
 FT DOMAIN 221 326 CH3.
 FT DOMAIN 327 457 CH4.
 FT DISULFID 13 13 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
 FT DISULFID 27 89 BY SIMILARITY.
 FT DISULFID 136 200 BY SIMILARITY.
 FT DISULFID 217 217 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 FT DISULFID 248 307 BY SIMILARITY.
 FT DISULFID 295 295 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 FT DISULFID 355 417 BY SIMILARITY.
 FT DISULFID 456 456 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 457 AA; 50074 MW; 56C8C086DA4462E9 CRC64;

Query Match 24.2%; Score 413.5; DB 1; Length 457;
 Best Local Similarity 30.1%; Pred. No. 8; le-26;

Matches 100; Conservative 58; Mismatches 157; Indels 17; Gaps 9;
 QY 3 PPTVKLIQSSQDGGGHPPTIQLCLVSGYTPGINTITWLEDQYMDVLDASTAQEGE 61
 Db 111 PPNVSLFVPPRNSGSGNHPRTSOLICQASFSPTTWSLQKEPQPSLVSAYEAE 170
 QY 62 ELAS-----TQSELTLSQKHWLSDRTTYQVVOYQGHFTPDSTKK--CADSNRGVSAYL 113
 Db 171 PKSGPTTFRVISLITTEENWLSQREFTOALHKLGTLPKNNVSVCMGSDTSTGISVFL 230
 QY 114 SRSPEDLFTFKSEPTTCLVVDLAPSKGYVNLWVSRAASKPVNHSTRKEKQNGTLTYT 173
 Db 231 LPPTFANIFLTQSOLCLVTGLA--TYSDSIDISRONGELQTHVNISESHNSTFTAK 289
 QY 174 STLPVGRDWIEGEGTCRYTHPLPRALMRSTTKTG--PRAAPEYAF--ATPEMPSRD 231
 Db 290 GHASVCREEWESGKEFTCYQHSDDLPSLKQSSRPKVDANDPVSFVLPPAEQQLKRE 349
 QY 232 KRTLACLIQNFMEPDISVQWLHNEVOLPDARHSTTQ---PRKTKSGFVEFSRLEVRAE 288
 Db 350 SASITCLVKNFSPDPVQVOMHHG--QPVDPKHVYTSMPTEPQNPGLTFVHSILTYSEKD 408
 QY 289 WEQKDEFFICRAVHEAASPSQTVORAVSVNPGK 320
 Db 409 WSSGSEFSFCVVGHEAL-PLSVTERKAVDKTSGK 439

RESULT 9
 MOCB_HUMAN
 ID MOCB_HUMAN STANDARD; PRT; 391 AA.
 AC P04220;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 1g mu heavy chain disease protein (BOT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=84184186; PubMed=6425189;
 RA Barnikol-Watanabe S., Mihaesco E., Mihaesco C., Barnikol H. U.,
 RA Hilschmann N.;
 RT "The primary structure of mu-chain-disease protein BOT. Peculiar
 RT amino-acid sequence of the N-terminal 42 positions.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 365:105-118(1984).
 CC -I- MISCELLANEOUS: THIS PROTEIN HAS NO V REGION HOMOMOLOGY OR CH1
 CC REGION.
 DR PIR: A02163; MHHDUT.
 DR HSSP: P01857; IFCL.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003600; Ig_like.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00410; Ig_like; 1.
 DR SMART: SM00407; Igcl; 2.
 DR PROSITE: PS00290; Ig_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT DOMAIN 1 42 PRE-C-PAFT (NO V REGION HOMOMOLOGY).
 FT DOMAIN 43 155 CH2.
 FT DOMAIN 156 261 CH3.
 FT DOMAIN 262 391 CH4.
 SO SEQUENCE 391 AA; 43057 MW; 9100843AF0CF021A CRC64;

Query Match 24.0%; Score 410; DB 1; Length 391;
 Best Local Similarity 28.6%; Pred. No. 1.3e-25;
 Matches 95; Conservative 61; Mismatches 156; Indels 20; Gaps 9;
 QY 3 PPTVKLIQSSQDGGGHPPTIQLCLVSGYTPGINTITWLEDQYMDVLDASTAQEGE 62
 Db 48 PPKVSVFVPPRNDGFFGNRKRSLICQATGSPROIENVSLREK-----QVGSVLTDEVE 103

OY 63 LASTO-----SELTSOKHMLSDRTYTCOVYOGHTF-EDSTKCKADSNPGVSAY 112
 DB 104 AEARESGPTTYKVTSTLTIKESDWSGSMFTCRVDHRLTFOQNASMCGPDODTAIRVF 163
 OY 113 LSRSPDFLTKRSPPTICLVADLAPSKGVNLWMSRSGKPVNHSRKEKORNGTLTV 172
 DB 164 AIPSPFASIFLTKSKTKLTCLVDTLT-TYDSVTISMTRODGAVKTHHTISSHPNATPSA 222
 OY 173 TSTLPVGTDMIESEYTCRVTHPLPALMRSTTKTSGPRA-AEYVYAF-ATPEWPGSR 230
 DB 223 VGEASICEDWDMSGERFTCTVTHDLPSPKLTISRPKGVALLHRPDVYLLPPARQULNR 282
 OY 231 DKRLACLIONFMEDISVQVLNHEVQLPDARHSTQPR-KTKSGG-FEVSRLKYTAE 288
 DB 283 ESAITTCVLTGFSPADVFWQWMOGQPLSPKRYTISAPMPPOAPGRYFAHSILTVSEEE 342
 OY 289 WEORDEFICRAVHEAASPTQVORAVSNPCK 320
 DB 343 WNTGETYCVVAHNEAL-PNRYTERTYDKSTCK 373
 RESULT 10
 MOC_HUMAN STANDARD: PRT: 454 AA.
 ID AC P01871;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ig mu chain C region.
 GN IGHM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 1-434 FROM N.A.
 RA MEDLINE=90332450; PubMed=2115996;
 RT Friedlander R.M., Nussenzweig M.C., Leder P.;
 RL "Complete nucleotide sequence of the membrane form of the human IgM
 heavy chain.";
 Nucleic Acids Res. 18:4278-4278(1990).
 RN [2]
 RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN GAL).
 RA MEDLINE=75059123; PubMed=4803843;
 RT Watanabe S., Barnikol H.U., Horn J., Berttram J., Hilschmann N.;
 RL "The primary structure of a monoclonal IgM-immunoglobulin
 (macroglobulin gal.), II: the amino acid sequence of the H-chain (mu-
 type), subgroup H III. Architecture of the complete IgM-molecule.";
 Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
 RN [3]
 RP REVISIONS (GAL).
 RA MEDLINE=81066716; PubMed=6777162;
 RT Milhaesco E., Barnikol-Watanabe S., Barnikol H.U., Milhaesco C.,
 RA Hilschmann N.;
 RL "The primary structure of the constant part of mu-chain-disease
 protein B0F.";
 Eur. J. Biochem. 111:275-286(1980).
 RN [4]
 RP SEQUENCE (WALDENSTROM'S O0), DISULFIDE BONDS, AND CARBOHYDRATES.
 RA MEDLINE=74005511; PubMed=4742735;
 RT Putnam F.W., Florent G., Paul C., Shinoda T., Shimitzu A.;
 RL "Complete amino acid sequence of the mu heavy chain of a human IgM
 immunoglobulin.";
 Science 182:287-291(1973).
 RN [5]
 RP PARTIAL SEQUENCE FROM N.A.
 RA MEDLINE=82059479; PubMed=6795593;
 RT Rabbitts T.H., Forster A., Milstein C.P.;
 RL "Human immunoglobulin heavy chain genes: evolutionary comparisons of
 C mu, C delta and C gamma genes and associated switch sequences.";
 Nucleic Acids Res. 9:4509-4524(1981).
 RN [6]
 RP SEQUENCE OF 299-387 AND 438-454 FROM N.A.

RX MEDLINE=81077306; PubMed=6777778;
 RA Dojby T.W., Devono J., Croce C.M.;
 RL "Cloning and partial nucleotide sequence of human immunoglobulin mu
 chain cDNA from B cells and mouse-human hybridomas.";
 Proc. Natl. Acad. Sci. U.S.A. 77:6027-6031(1980).
 CC -1- MISCELLANEOUS: ALL 4 COMBINATIONS OF THE S/G & V/G POLYMORPHISMS
 AT POSITIONS 192 AND 216 HAVE BEEN OBSERVED IN HUMAN MU CHAINS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X17115; CAA34971.1; ALT_SEQ.
 DR EMBL: X57086; -: NOT_ANNOTATED_CDS
 DR PIR: A02182; MHU.
 DR HSSP: P01857; IFC1.
 DR GeneW: HGNC:5541; IGHM.
 DR MIM: 147020;
 DR GlycosultedB: P01871;
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig-cl.
 DR InterPro: IPR003600; Ig_like.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00410; Ig_Like; 1.
 DR SMART: SM00407; IGL; 3.
 DR PROSITE: PS00290; Ig_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1
 FT DOMAIN 1
 FT DOMAIN 106 105
 FT DOMAIN 219 218
 FT DOMAIN 325 324
 FT DOMAIN 325 454
 FT DISULFID 14 14
 FT DISULFID 28 88
 FT DISULFID 135 198
 FT DISULFID 215 215
 FT DISULFID 245 304
 FT DISULFID 292 292
 FT INTERCHAIN (WITH A HEAVY CHAIN).
 FT INTERCHAIN (WITH A HEAVY CHAIN IN ANOTHER
 OF THE 5 TETRAMERIC SUBUNITS OF THE
 MOLECULE).
 FT DISULFID 352 414
 FT DISULFID 453 453
 FT CARBOHYD 46 46
 FT CARBOHYD 210 210
 FT CARBOHYD 273 273
 FT CARBOHYD 280 280
 FT CARBOHYD 441 441
 FT VARIANT 192 192
 FT VARIANT 192 192
 FT VARIANT 216 216
 FT VARIANT 216 216
 FT SEQUENCE 454 AA; 49556 MW; 21EC72EADC56922E CRC64;
 SQ
 Query Match 23.8%; Score 405.5; DB-1; Length 454;
 Best Local Similarity 28.6%; Pred. No. 3.5e-25;
 Matches 94; Conservative 64; Mismatches 158; Indels 13; Gaps 9;
 OY 3 PPTVYKLIQSSCDG-GGHEPPTIQLCLVSGYTPGTINITWLEDQGVNDVLSASTQEG 61
 DB 110 PKPVSVFVPPRDPDFGPNRSKSKLICATGFSFROIQVSWLREKQVGSVTTDOVQAEA 169
 OY 62 ELA-----STSELTLSOKHMLSDRTYTCOVYOGHTF-EDSTKCKADSNPGVSATL 115
 DB 170 KESGPTTYKVTSTLTIKESDWSGSMFTCRVDHRLTFOQNASMCGPDODTAIRFAIP 229
 OY 116 PSPDFLTKRSPPTICLVADLAPSKGVNLWMSRSGKPVNHSRKEKORNGTLTVTST 175
 DB 230 PSFASIFLTKSKTKLTCLVDTLT-TYDSVTISMTRODGAVKTHHTISSHPNATPSA 288

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QY 176 LPVGTQRMIEGETYQCRTHPHLRALMRSTKTSQGRA-APEYVAF-ATPEMFGSNDKR 233
D 289 ASIEDDMNSGERCTVTHDLPSPKQITSRKGVALLHPDDVYLLPPAREQNLRESA 348
QY 234 TLACIIONMPEIDISVOMLHNEVOLPDARHSTQPR-KTKGSG-FEVSRLRYRAEEO 291
D 349 TITLVGTFSPADVFVQMGQGPLSPKRYTSPADPEPPQAGRFHSHILTVSEEWNT 408
QY 292 KDEFCIRAVHEASPSQTVQRAVSVPNGK 320
D 409 GETTCVAHEAL-PNRYTERTVDKSTGK 436

RESULT 11
MUC_RABIT STANDARD: PRT: 458 AA.
ID MUC_RABIT STANDARD: PRT: 458 AA.
AC P03988:
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig mu chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A. (A2 ALLOTYPE).
RX MEDLINE=84088930; PubMed=6418803;
RA Bernstein K.E., Alexander C.B., Reddy E.P., Mage R.G.;
RT "Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain
  of Vha2 allotype: comparisons with Vha1 and membrane mu sequences.";
RL J. Immunol. 132:490-495(1984).
-1- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCYTES
  SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF IGM.
  THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C-
  TERMINAL SEGMENTS.
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  or send an email to license@sdb.ch).
CC -----
DR EMBL: K01357; -; NOT_ANNOTATED_CDS.
DR PIR: A02164; MHRB.
DR HSSP: P01842; 7EAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig_4.
DR SMART: SMO0410; Ig_Like; 2.
DR SMART: SMO0407; IGc1; 2.
DR PROSITE: PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing.
FT DOMAIN 1 106 CH1.
FT DOMAIN 107 222 CH2.
FT DOMAIN 223 327 CH3.
FT DOMAIN 328 458 CH4.
FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
FT DISULFID 28 90 BY SIMILARITY.
FT DISULFID 137 200 BY SIMILARITY.
FT DISULFID 219 219 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 249 308 BY SIMILARITY.
FT DISULFID 296 296 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 356 418 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 458 AA; 49897 MW; F338D6A3828E4864 CMC64;

Query Match 23.8%; Score 405.5; DB 1; Length 458;
Best Local Similarity 30.0%; Pred. No. 3.6e-25;
Matches 100; Conservative 60; Mismatches 154; Indels 19; Gaps 10;

QY 3 PPTVKIL---OSSODGGGHPPTIOLCLVSGYRGNTINWLEDGOVMDVLTASTQ 59
D 112 PPNVSVLTPPDSTSGSG--TRKSRLQATGSEKQISWLDGQKVEGLTKPYEA 169
QY 60 EGELA-----STOSELTLQKHWLSDRTTYQCVYQGHTEFDS--TKKCADSNRGVSA 111
D 170 ETKGAGPATFSSMLTTTESDMLQSOLYTCRVDRHGIFFPKNNMSSECTTSPGLOV 229
QY 112 YLSRSPEDLFIKRSPTITCLVLDLASKGTAVNLTWASASGPVNNHSTRKEKORNGTLT 171
D 230 FPIAPSPADTFLSKRSARLCLVDTLT-TYGSINISWASHNKAADTHNITESHNPATFS 288
QY 172 VTSTLPVGTQRMIEGETYQCRTHPHLRALMRSTKT-SGPRAAPEYVAF-ATPEMFGS 229
D 289 AMGEASVCAEDWESGEQFTCTVHADLPFLKHTISREYAKHPPAVTVLPAREQLVL 348
QY 230 RDKRTLACIIONMPEIDISVOMLHNEVOLPDARHSTQPR-KTKGSG-FEVSRLRYTRA 287
D 349 RESATVETLVGTFSPADVFVQMGQGPLSSDKTYTSAPAREPPAGLYFHSHTLVTEE 408
QY 288 EWEQKDEFTICRAVHEASPSQTVQRAVSVPNGK 320
D 409 DWNSEFTTCVAGHEAL-PNRYTERTVDKSTGK 440

RESULT 12
GC2_CAVPO STANDARD: PRT: 329 AA.
ID GC2_CAVPO STANDARD: PRT: 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.
CC NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (Apr-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
  immunoglobulin-G(2). 3. Amino acid sequence of the region around the
  half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
  immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
  and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
  antibodies.";

```

RL Biochemistry 13:4796-4803(1974).
 RN [5]
 RP SEQUENCE OF 227-311.
 RX MEDLINE=75036073; PubMed=4609467;
 RA Trischmann T.M., Cebra J.J.;
 RT "Primary structure of the CH3 homology region from guinea pig IgG2
 antibodies";
 RL Biochemistry 13:4804-4811(1974).
 RN [6]
 RP DISULFIDE BONDS.
 RX MEDLINE=71058474; PubMed=4922544;
 RA Oliveira B., Lam M.E.;
 RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
 RL Biochemistry 10:26-31(1971).
 CC -1 MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
 CC 13 INBRED GUINEA PIGS.
 DR PIR: A02151; GZGP.
 DR HSSP: P01842; 7FAB.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003597; IG-cl.
 DR InterPro: IPR003600; IG-like.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00410; IG-like; 1.
 DR SMART: SM00407; IGcl; 2.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1
 FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 28 79
 FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 142 202
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
 FT DISULFID 248 308
 SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;
 Query Match 23.7%; Score 404.5; DB 1; Length 329;
 Best Local Similarity 30.6%; Pred. No. 2.8e-25;
 Matches 106; Conservative 56; Mismatches 135; Indels 49; Gaps 13;
 QY 2 TPPTVKILQSSC-DGGGHFPPTIQLCLVSGYPTGTITWLEDOGVADVLDSTASTQ 60
 DB 5 TAPSVFLPAAACVDTSGSM--MTLGLVKGYPPEPVTKV--NSGALTSVTHFPAVLQ 59
 QY 61 GELASTOSELTLSKHKHMLSDRTTCQVLYOCHTFEDSK-----KC 101
 DB 60 SGLTSLTSMVTP-----SSQKATCVNAHPA-----STKVDKTVPIRTPBPCTCPKC 110
 QY 102 -ADSNPGVSAVLSRSPFD-LFIRKSPITCLVVDLAPSKGTNLTMSRASGKV-NHS 158
 DB 111 PPENLGGPSVFIFPPPKDILMLSLPRVYCVVVDVSODEPEVQFTWF-VDNKPVGNAE 169
 QY 159 TRKEEKORNGTLIVTSLPVGTRDMIGETVQCRAVTHPLRALMRSTTKTSGRAAEV 218
 DB 170 TKPEVEQYNTTFREVSFLPIQHDMLRKGKCKYKNAKLPAPLEKTIISKTKGAPRMDV 229
 QY 219 YAFATPMPGSRD-----KRTLACLIONFMEPDISVOMLHNEVOLDPAHSTTPPKTKG 273
 DB 230 YTL-----PPSRDLSSKVASVLTLLINFPADLHVEWASRYVSVSEKYNTPEDDAD 284
 QY 274 SGFEVSRLEVTAEWQKDEFLICRAVHAASPSQFQRAVSNVP 319
 DB 285 GSYFLYSKRLVYDKSAMQGTIVYTCVSHALH-NHYTOKAISRSPG 329

DE Ig gamma-1 chain C region.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80045036; PubMed=115593;
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
 gamma 1 chain gene";
 RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
 RX MEDLINE=80202559; PubMed=6769752;
 RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
 RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
 RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
 cloned in a bacterial plasmid.";
 RL Gene 9:87-97(1980).
 RN [3]
 RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=80012837; PubMed=113776;
 RA Rogers J., Clarke P., Salsner W.;
 RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
 heavy chain.";
 RL Nucleic Acids Res. 6:3305-3321(1979).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=78242288; PubMed=98524;
 RA Adetugbo K.;
 RT "Evolution of immunoglobulin subclasses. Primary structure of a
 murine myeloma gamma1 chain.";
 RL J. Biol. Chem. 253:6068-6075(1978).
 RN [5]
 RP DISULFIDE BONDS (MOPC 21).
 RX MEDLINE=73008889; PubMed=5073237;
 RA Svasti J., Milstein C.;
 RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
 RL Biochem. J. 126:837-850(1972).
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 CC -----
 DR EMBL: V00793; CAA24172.1; -
 DR EMBL: V00793; CAA24173.1; -
 DR EMBL: V00793; CAA24174.1; -
 DR EMBL: V00793; CAA24175.1; -
 DR EMBL: V00795; CAA24176.1; -
 DR PIR: A02159; GIMS.
 DR HSSP: P01842; 7FAB.
 DR GlycoSuiteDB: P01868; -
 DR MGD: MGI:96446; Igh-4.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003597; IG-cl.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00407; Igcl; 2.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing.
 FT NON_TER 1
 FT DOMAIN 1 97
 FT DOMAIN 98 110 CH1.
 FT DOMAIN 111 217 HINGE.
 FT DOMAIN 218 324 CH2.
 FT DISULFID 27 82 CH3.
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).

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FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CAROHND 174 174 N-LINKED (GLCNAc. . .).
FT DISULFID 244 302 /FTID=CAR_000035.
FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
FT CONFLICT 276 276 N -> D (IN REF. 3).
FT CONFLICT 278 278 N -> D (IN REF. 3).
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1FC93 CRC64;

Query Match 23.6%; Score 402; DB 1; Length 324;
Best Local Similarity 29.2%; Pred. No. 4.4e-25;
Matches 96; Conservative 60; Mismatches 155; Indels 18; Gaps 7;

QY 2 TPPIYKIIQSSCDGGHPPTIQLCLVSGYTPGINTITWLEDGVMVDLSTASTQBG 61
DB 4 TPPIYKIIQSSCDGGHPPTIQLCLVSGYTPGINTITWLEDGVMVDLSTASTQBG 59
QY 62 ELASTQSELTLSQKHWLSDRTYTCOVYQGHTE-----EDSTKKCADSNPRGVSAY 112
DB 60 DLYTLSSSVTVPPSSRPSSE-IVTCNVNAPASTKTKDKIIVPRDCGCKFCICVPEVSSVF 118
QY 113 LSRPSPEP-LFTRKSPITTCVLVDLAPSKGVNLTWSRASKGVNHSRTRKEKQKNGTLT 171
DB 119 IFPPKPKDVLITTLTPKVTGVVDISKDDPEVQSFVDDVEVHTAQTPRDEQNSTFR 178
QY 172 VTSTLPVGTIRMIBETVOCRTNPHLPRALMRSTTKSGPRAAEVYAFAPPEPGSD 231
DB 179 SVSELPIMHODWLNKEKFCRNASAPAPLEKTIKTKGRPKAQVYVITPPPKQMAKD 238
QY 232 KRTIACLIQNPEDISVQWLNHEVQLPDARHSTQPKTKSGFVFSRLTEVRAEMEQ 291
DB 239 KVSILCMITDPEPEDIYEMQMN--GQPAENKKNQPIIMNTNGSFVYSKLNWQSNMBA 296
QY 292 KDEFTICRAVHEAPSPQTVQRAVSNPK 320
DB 297 GNTFTCSVILHGLNHNHT-EKSLSHSPK 324

RESULT 14
GCAL_MOUSE STANDARD; PRT; 330 AA.
ID GCAL_MOUSE
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-2a chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Sikoray J.-L., Auftray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT Balb/c gamma 2a heavy chain messenger RNA."
RL Nucleic Acids Res. 8:3143-3155(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RT and evolution of heavy chain genes: further evidence for intervening
RT sequence-mediated domain transfer."
RL Nucleic Acids Res. 9:1365-1381(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81223894; PubMed=6787604;
RA Olio R., Auftray C., Morchamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes

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RT suggests that exons can be exchanged between genes in a multigenic
RT family."
RT Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin: amino acid sequence of the FC fragment. Implications
RT for the evolution of immunoglobulin structure and function."
RL Eur. J. Biochem. 43:423-435(1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges."
RL Eur. J. Biochem. 30:452-462(1972).
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: V00758; CAA24178.1; -
DR PIR: A02192; G2MSA.
DR HSP: P01842; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig_2
DR SMART: SM00410; Ig_Like; 1.
DR SMART: SM00407; IgC1; 2.
DR PROSITE: PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C545A6864 CRC64;

Query Match 23.4%; Score 399; DB 1; Length 330;
Best Local Similarity 28.6%; Pred. No. 7.8e-25;
Matches 97; Conservative 62; Mismatches 146; Indels 32; Gaps 8;

QY 2 TPPIYKIIQSSCDGGHPPTIQLCLVSGYTPGINTITWLEDGVMVDLSTASTQBG 61
DB 4 TPPIYKIIQSSCDGGHPPTIQLCLVSGYTPGINTITWLEDGVMVDLSTASTQBG 59
QY 62 ELASTQSELTLSQKHWLSDRTYTCOVYQGHTE-----EDSTKKCADSNPRGVSAY 111
DB 60 DLYTLSSSVTVPPSSRPSSE-IVTCNVNAPASTKTKDKIIVPRDCGCKFCICVPEVSSVF 114
QY 112 --YLSRPSPE-----DLFTRKSPITTCVLVDLAPSKGVNLTWSRASKGVNHSRTRK 161
DB 115 PALLGSPSFIIPPKIKDVLIMSLPIYTCVVVDSEDDPDQISMFVNANVEVHTAQGT 174
QY 162 EKQKNGITLVSTLPVGTROMIEBETVOCRTNPHLPRALMRSTTKSGPRAAEVYAF 221
DB 175 HREDNSTLRVVSALPIQHDWMSGKERCKKNNNDLPAPERTSKTKSGVRAQVYVL 234
QY 222 APPEWPGSRDKRTIACLIQNPEDISVQWLNHEVQLPDARHSTQPKTKSGFVFSR 281
DB 235 PPPEEMTKKQVTLTCMTDPEPEDIYEMQMN--GKTELANKTEPVLDSGYSFTSK 292

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FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 240
FT TURN 241 242
FT STRAND 245 256
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FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match

23.3%; Score 397.5; DB 1; Length 330;

Best Local Similarity 31.0%; Pred. No. 1e-24;

Matches 102; Conservative 54; Mismatches 138; Indels 35; Gaps 10;

QY 12 SCGGGHEPPTIQLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGELASTOSELT 71
DB 17 STGGG-----TALGCLVKDYFPEPVTVSW-NSGALTSGVHTFPFAVLQSSGLYSLSSVT 70
QY 72 LSKHMLSDRTYTCQVYYOCHTE-----DSTKGC---ADSNPRGVSAIYLSRPS 117
DB 71 VPSSS-LGTQTYICNVNHNKPSNTRKVDKRVKPKSCDKTHTCPCPAPPELLGGPSVFLP 129
QY 118 PFD-LFIRKSPITTCLVVDLAPSKGVNLTWSRASKPVNHNSTRKEEKORNGTLTVSTL 176
DB 130 PKDTLMSRPEYTCVVDVSHEDPEYKEMWYVDGVYHNAKTKPREQYINSTYRYSVL 189
QY 177 PVGTDMIEGETYQCRVTHPLPALMSTTKTSGPRAAPEVYAFAPEWPGSRDKRT-- 234
DB 190 TVLHODVLNGEKYCKSNKALPAPIETISKAKGPPEPVYTL-----PPSRDELTKN 244
QY 235 ---LACLIQNPMPEDISVOMLHNEVQLPDARHSTTOPRKTGSGGFVFSRLEVTRAMEQ 291
DB 245 QVSLTCLVKGFPYSDIHAVEMESN--GQPENNYKTPPVLDSDGSFELYSKLTVDKSRWQ 302
QY 292 KDEFICRAVHEAASPSQTVORAVSVNPGK 320
DB 303 GNVFSCSVMHMALHNHT-QKSLSLSPRK 330

Search completed: July 15, 2003, 06:58:20
Job time : 10.9911 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:46:49 ; Search time 37.6806 Seconds
(without alignments)
1131.621 Million cell updates/sec

Title: US-09-847-208B-6

Perfect score: 1707
Sequence: 1 FRPPTVKIIQSSCDGGGHPF.....HEAAPSQTVQRAVSNPKG 320

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|-------------|
| 1 | 1707 | 100.0 | 323 | AAU80284 |
| 2 | 1707 | 100.0 | 323 | AAU80285 |
| 3 | 1707 | 100.0 | 323 | AAU80286 |
| 4 | 1707 | 100.0 | 324 | AAU80287 |
| 5 | 1707 | 100.0 | 325 | AAU80288 |
| 6 | 1707 | 100.0 | 325 | AAU80289 |
| 7 | 1707 | 100.0 | 331 | AAU80290 |
| 8 | 1707 | 100.0 | 367 | AAU80291 |
| 9 | 1707 | 100.0 | 428 | AAU80283 |
| 10 | 1707 | 100.0 | 428 | AAU80284 |

| | | | | | |
|----|--------|-------|-----|-----------|----------------------|
| 11 | 1707 | 100.0 | 428 | AAU47863 | Human Ig-E heavy C |
| 12 | 1701 | 99.6 | 325 | AAU79994 | Human immunoglobulin |
| 13 | 1696 | 99.4 | 336 | AAU80288 | Human IgE heavy ch |
| 14 | 1696 | 99.4 | 441 | AAU80287 | Human IgE heavy ch |
| 15 | 1693 | 99.2 | 493 | AAU40065 | Sequence of human |
| 16 | 1685 | 98.7 | 325 | AAU83582 | CH2 to CH4 of huma |
| 17 | 1677 | 98.2 | 315 | AAU85582 | Fc(epsilon) CH2'-C |
| 18 | 1671 | 97.9 | 330 | AAU80289 | Human IgE C2-C3-C4 |
| 19 | 1663 | 97.4 | 428 | AAU82950 | Human IgE heavy ch |
| 20 | 1158 | 67.8 | 218 | AAU85583 | Fc(epsilon) CH2'-C |
| 21 | 1158 | 67.8 | 222 | AAU85589 | Amino acid sequenc |
| 22 | 1088 | 63.7 | 201 | AAU85589 | Fc(epsilon) CH2'-C |
| 23 | 1038.5 | 60.8 | 342 | AAU806205 | Immunogenic peptid |
| 24 | 1038 | 60.8 | 209 | AAU90010 | Residues 340-547 o |
| 25 | 1013 | 59.3 | 190 | AAU85584 | Fc(epsilon) CH2'-C |
| 26 | 948.5 | 55.6 | 426 | AAU87753 | Canine IgE. Canis |
| 27 | 945 | 55.4 | 424 | AAU80103 | Equine IgE heavy C |
| 28 | 943 | 55.2 | 424 | AAU50104 | Equine IgE heavy C |
| 29 | 928.5 | 54.4 | 417 | AAU23067 | Canine IgE heavy C |
| 30 | 895.5 | 52.5 | 312 | AAU79995 | Dog immunoglobulin |
| 31 | 827 | 48.4 | 341 | AAU806208 | Immunogenic peptid |
| 32 | 793 | 46.5 | 340 | AAU83643 | Rat IgE heavy chal |
| 33 | 783 | 45.9 | 313 | AAU79996 | Rat immunoglobulin |
| 34 | 781 | 45.8 | 341 | AAU83644 | Opossum IgE heavy C |
| 35 | 770 | 45.1 | 345 | AAU806207 | Immunogenic peptid |
| 36 | 751 | 44.0 | 332 | AAU80297 | Mouse IgE heavy ch |
| 37 | 751 | 44.0 | 332 | AAU80298 | Mouse IgE heavy C |
| 38 | 751 | 44.0 | 332 | AAU80299 | Mouse IgE heavy C |
| 39 | 751 | 44.0 | 341 | AAU806206 | Immunogenic peptid |
| 40 | 751 | 44.0 | 421 | AAU80300 | Mouse IgE heavy ch |
| 41 | 748 | 43.8 | 343 | AAU80295 | Murine IgE heavy C |
| 42 | 748 | 43.8 | 343 | AAU80296 | Murine IgE heavy C |
| 43 | 748 | 43.8 | 432 | AAU80294 | Murine IgE heavy C |
| 44 | 695 | 40.7 | 130 | AAU85585 | Fc(epsilon) CH2'-C |
| 45 | 691.5 | 40.5 | 313 | AAU79997 | Mouse immunoglobul |

ALIGNMENTS

| | | |
|----------|---|----------------------------|
| RESULT 1 | AAU80284 | standard; Protein; 323 AA. |
| ID | AAU80284 | |
| XX | AAU80284 | |
| AC | AAU80284 | |
| XX | 30-JUL-2002 | (first entry) |
| XX | Human IgE heavy chain C2-C3-C4 domains. | |
| DE | Human IgE heavy chain C2-C3-C4 domains. | |
| XX | IgE: allergen; human; antiallergic; immunosuppressive; antiaphyllactic; | |
| XX | antiallergic; dermatological; anti-inflammatory; immunoglobulin E; IgE; | |
| KW | vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis; | |
| KW | heavy chain C domain. | |
| XX | Homo sapiens. | |
| OS | Homo sapiens. | |
| XX | Key | |
| FH | Domain | |
| FT | Domain | |
| FT | Region | |
| FT | Region | |
| FT | Region | |
| FT | Region | |
| FT | Region | |
| FT | Region | |
| FT | Domain | |
| FT | Region | |

Location/Qualifiers
8..103 "IgE heavy chain C2 domain"
100..114 "IgE heavy chain C3 domain"
104..111 "Epitope including C2C3 linker"
112..211 "Linker between domains C2 and C3"
139..145 "label= IgE heavy chain C3 domain"
167..175 "note= "Epitope in BC loop"
196..206 "note= "Epitope in DE loop"
210..218 "note= "Epitope in FG loop"

| FT | Region | /note="Epitope including C3C4 linker" |
|----|--|--|
| FT | 212..215 | /note="Linker between domains C3 and C4" |
| FT | 216..317 | /note="IgE heavy chain C4 domain" |
| FT | Domain | |
| PN | WO200220038-A2. | |
| XX | 14-MAR-2002. | |
| XX | 06-SEP-2001; 2001WO-DK00579. | |
| XX | 06-SEP-2000; 2000DK-0001326. | |
| XX | 15-SEP-2000; 2000US-232831P. | |
| XX | (PHAR-) PHARMEXA AS. | |
| XX | Klysner S, Von Hoegen P, Voldborg B, Gautam A; | |
| XX | WPI: 2002-383033/41. | |
| DR | | |
| XX | | |
| PT | Inducing immune response against autologous immunoglobulin E in an | |
| PT | animal, by effecting simultaneous presentation of cytotoxic T | |
| PT | lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin | |
| PT | - | |
| XX | | |
| PS | Disclosure: Page 105-106; 151pp; English. | |
| XX | | |
| CC | This invention relates to a novel method for inducing an immune response | |
| CC | against autologous immunoglobulin E (IGE) in an animal. The method | |
| CC | comprises effecting simultaneous presentation of cytotoxic T lymphocyte | |
| CC | (CTL) epitope and/or B-cell epitope derived from IGE, and T helper cell | |
| CC | epitope (TH epitope) which is foreign to the animal, by antigen | |
| CC | presenting cells (APCs) of the animal's immune system. The epitopes | |
| CC | of the invention may be used as a vaccine against allergic diseases. The | |
| CC | method of the invention is useful for inducing an immune response | |
| CC | against autologous IGE in an animal, which is useful for downregulating | |
| CC | autologous IGE in the animal. This method is useful in the prevention | |
| CC | and treatment of allergic diseases such as anaphylaxis, allergic | |
| CC | rinitis, asthma and atopic dermatitis. The present sequence represents | |
| CC | the human IGE heavy chain C2-C3-C4 domains used to create the | |
| CC | epitopes of the invention. | |
| XX | | |
| XX | Sequence 323 AA; | |
| QY | Query Match | 100.0%; Score 1707; DB 23; Length 323; |
| Db | Best Local Similarity | 100.0%; Pred. No. 1,1e-129; |
| Yy | Matches 320; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; |
| QY | 1 FTPTPTVAILLSSCGGCHFPPTIQLCLVSGYPTGCTINITWLEBQGVMDVLSTASTQOE | 60 |
| Db | 4 FTPTPTVAILLSSCGGCHFPPTIQLCLVSGYPTGCTINITWLEBQGVMDVLSTASTQOE | 63 |
| Yy | 61 GELASTOSELTLSOKHMLSDRTYTCQVYTGHTFEDSTKCADSNRGVSAYLNSPSPD | 120 |
| Db | 64 GELASTOSELTLSOKHMLSDRTYTCQVYTGHTFEDSTKCADSNRGVSAYLNSPSPD | 123 |
| QY | 121 LFIKRSPTITCLVVDLAPSKCTVNLWTSRAGKRVNHNSTKKEEQRNGCTLVITSTLPVGT | 180 |
| Db | 124 LFIKRSPTITCLVVDLAPSKCTVNLWTSRAGKRVNHNSTKKEEQRNGCTLVITSTLPVGT | 183 |
| QY | 181 RDMIEGEGTYOCRWVHPLPRALMSTKTSQSPRAPEVYARAPPEWPSRKRFLACIQ | 240 |
| Db | 184 RDMIEGEGTYOCRWVHPLPRALMSTKTSQSPRAPEVYARAPPEWPSRKRFLACIQ | 243 |
| QY | 241 NFMEDISYVWLHNEVOLPDARHSTQPRKTKSGGFVFSRLFETVTRAEWEDKDFICRAV | 300 |
| Db | 244 NFMEDISYVWLHNEVOLPDARHSTQPRKTKSGGFVFSRLFETVTRAEWEDKDFICRAV | 303 |
| QY | 301 HEAASPSQTYQRAVSVPNGK 320 | |
| Db | 304 HEAASPSQTYQRAVSVPNGK 323 | |

| ID | AA#080285 | standard; Protein; 323 AA. |
|----|--------------------------------------|---|
| XX | AA080285; | |
| XX | 30-JUL-2002 | (first entry) |
| XX | Human Ige C2-C3-C4 domains | for mammalian expression. |
| XX | Ige: allergy; human; antiallergic; | immunosuppressive; antianaphylactic; |
| XX | antihistaminic; dermatological; | antiinflammatory; immunoglobulin E; Ige; |
| XX | vaccine; anaphylaxis; allergic | rinitis; asthma; atopic dermatitis; |
| XX | heavy chain C domain. | |
| OS | Homo sapiens. | |
| OS | Synthetic. | |
| PN | WO200220038-A2. | |
| XX | 14-MAR-2002. | |
| XX | 06-SEP-2001; 2001WO-DK00579. | |
| XX | 06-SEP-2000; 2000DK-0001326. | |
| XX | 15-SEP-2000; 2000US-232831P. | |
| XX | (PHAR-) PHARMEXA AS. | |
| XX | Klysnar S, Von Hoegen P, Voldborg B, | Gautam A; |
| XX | WPI: 2002-383033/41. | |
| XX | N-PSDB: ABK51133. | |
| XX | Inducing immune response against | autologous immunoglobulin E in an |
| XX | animal, by effecting simultaneous | presentation of cytotoxic T |
| XX | lymphocyte epitope an/or B-cell | epitope derived from the immunoglobulin |
| XX | disclosure; Page 108-110; 151pp; | English. |
| XX | This invention relates to a novel | method for inducing an immune response |
| XX | against autologous immunoglobulin | E (Ige) in an animal. The method |
| XX | comprises effecting simultaneous | presentation of cytotoxic T lymphocyte |
| XX | (CTL) epitope and/or B-cell | epitope derived from Ige, and T helper cell |
| XX | epitope (TH epitope) which is | foreign to the animal, by antigen |
| XX | presenting cells (APCs) of the | animal's immune system. The epitopes |
| XX | of the invention may be used as | a vaccine against allergic diseases. The |
| XX | method of the invention is useful | for inducing an immune response |
| XX | against autologous Ige in an | animal, which is useful for downregulating |
| XX | autologous Ige in the animal. | This method is useful in the prevention |
| XX | and treatment of allergic | diseases such as anaphylaxis, allergic |
| XX | rinitis, asthma and atopic | dermatitis. The present sequence |
| XX | represents the human Ige heavy | chain C2-C3-C4 domains optimised for |
| XX | expression in a mammalian | system, this sequence was used to |
| XX | create the epitopes of the | invention. |
| XX | Sequence 323 AA: | |
| XX | Query Match 100.0%; Score 1707; | DB 23; Length 323; |
| XX | Best Local Similarity 100.0%; | Pred. No. 1,1e-129; |
| XX | Matches 320; Conservative 0; | Mismatches 0; Indels 0; Gaps 0 |
| XX | 1 FPPPYKIIQSSDDGGHPPPTIQLCLVSGT | PTINITWLEGGQVNDVLSASTQOE 60 |
| XX | 4 FPPPYKIIQSSDDGGHPPPTIQLCLVSGT | PTINITWLEGGQVNDVLSASTQOE 63 |
| XX | 61 GELASTQSELTLISQKHWLSDRYTQVY | YQGHTEFEDSTRKCADSNPGVSAYLSRPSFD 120 |
| XX | 64 GELASTQSELTLISQKHWLSDRYTQVY | YQGHTEFEDSTRKCADSNPGVSAYLSRPSFD 123 |
| XX | 121 LPIRKSPTITCLVNDLAPSKGTVNL | TWSBRASGPNVNHSTRKEERKORNGTLTVTSTLPVGT 1800 |

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Db      124  LFIKSPITICLVVDLAPSKGVTLTWSRASGKPVNSTRKEEKORNGTLTVSTLPVGT 183
Qy      181  RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAAPEVYAFATPEWGSRDKRTLACLIQ 240
Db      184  RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAAPEVYAFATPEWGSRDKRTLACLIQ 243
Qy      241  NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFFVFSRLVETRAEMEQKDEFICRAV 300
Db      244  NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFFVFSRLVETRAEMEQKDEFICRAV 303
Qy      301  HEASPSQTVQRAVSVNPGK 320
Db      304  HEASPSQTVQRAVSVNPGK 323

RESULT 3
AA080286
ID      AA080286 standard; Protein: 323 AA.
XX
AC      AA080286;
XX
DT      30-JUL-2002 (first entry)
XX
DE      Human Ige C2-C3-C4 domains for E.Coli expression.
XX
KW      IGF: allergy; human; antiallergic; immunosuppressive; antiaphylactic;
KW      antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; Ige;
KW      vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
KW      heavy chain C domain.
XX
OS      Homo sapiens.
XX
SS      Synthetic.
XX
PN      W0200220038-A2.
XX
PD      14-MAR-2002.
XX
PE      06-SEP-2001; 2001WO-DK00579.
XX
PR      06-SEP-2000; 2000DK-0001326.
XX
PR      15-SEP-2000; 2000US-232831P.
XX
PA      (PHAR-) PHARMEXA AS.
XX
PI      Klysner S, Von Hoegen P, Voldborg B, Gautam A;
XX
DR      WPI: 2002-383033/41.
DR      N-PSDB: ABR51134.
XX
PT      Inducing immune response against autologous immunoglobulin E in an
PT      animal, by effecting simultaneous presentation of cytotoxic T
PT      lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
PT      .
XX
XX      Disclosure: Page 112-113; 151pp; English.
XX
XX      This invention relates to a novel method for inducing an immune response
XX      against autologous immunoglobulin E (Ige) in an animal. The method
XX      comprises effecting simultaneous presentation of cytotoxic T lymphocyte
XX      (CTL) epitope and/or B-cell epitope derived from Ige, and T helper cell
XX      epitope (TH epitope) which is foreign to the animal, by antigen
XX      presenting cells (APCs) of the animal's immune system. The epitopes
XX      of the invention may be used as a vaccine against allergic diseases. The
XX      method of the invention is useful for inducing an immune response
XX      against autologous Ige in an animal, which is useful for downregulating
XX      autologous Ige in the animal. This method is useful in the prevention
XX      and treatment of allergic diseases such as anaphylaxis, allergic
XX      rhinitis, asthma and atopic dermatitis. The present sequence represents
XX      the human Ige heavy chain C2-C3-C4 domains optimised for expression in
XX      an E. Coli system, this sequence was used to create the epitopes of the
XX      invention.

```

```

SQ      Sequence      323 AA;
Query Match      100.0%; Score 1707; DB 23; Length 323;
Best Local Similarity 100.0%; Pred. No. 1,1e-129;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  FTPTVAILQSSCDGGHFPPTIQLCLVSGYPTGTINITWLEDGYMDVDLSTASTTQE 60
Db      4  FTPTVAILQSSCDGGHFPPTIQLCLVSGYPTGTINITWLEDGYMDVDLSTASTTQE 63
Qy      61  GELASTQSELTLSCKHMLSDRTTYCOVYYQGHTEDESTKCCADSNPGVSATYLSRSPFD 120
Db      64  GELASTQSELTLSCKHMLSDRTTYCOVYYQGHTEDESTKCCADSNPGVSATYLSRSPFD 123
Qy      121  LFIKSPITICLVVDLAPSKGVTLTWSRASGKPVNSTRKEEKORNGTLTVSTLPVGT 180
Db      124  LFIKSPITICLVVDLAPSKGVTLTWSRASGKPVNSTRKEEKORNGTLTVSTLPVGT 183
Qy      181  RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAAPEVYAFATPEWGSRDKRTLACLIQ 240
Db      184  RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAAPEVYAFATPEWGSRDKRTLACLIQ 243
Qy      241  NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFFVFSRLVETRAEMEQKDEFICRAV 300
Db      244  NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFFVFSRLVETRAEMEQKDEFICRAV 303
Qy      301  HEASPSQTVQRAVSVNPGK 320
Db      304  HEASPSQTVQRAVSVNPGK 323

RESULT 4
AAR83559
ID      AAR83559 standard; Protein: 324 AA.
XX
AC      AAR83559;
XX
DT      06-MAR-1996 (first entry)
XX
DE      Fc(epsilon)-CH2'-CH4' protein-sequence.
XX
KW      Fc(epsilon); antibody; human; myeloma; probe; Ige; tryptophan promoter;
KW      constant heavy region; E.coli; glycosylation; antigenic; immunogenic;
KW      histamine; anti-allergenic; vaccine; immune response.
XX
OS      Synthetic.
XX
PN      FR2715304-A1
XX
PD      28-JUL-1995.
XX
PE      26-JAN-1994; 94FR-0000846.
XX
PR      26-JAN-1994; 94FR-0000846.
XX
PA      (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.
XX
PI      Hurpin CM, Panero MJM;
XX
DR      WPI: 1995-265243/35.
DR      N-PSDB: AAT01865.
XX
PT      Antiallergic vaccine contg. polypeptide fragment of Ige heavy chain
PT      - has epitope(s) not present in native Ige, also derived antibodies
PT      for treating or preventing allergies, inflammatory immune disease,
PT      etc.
XX
XX      Claim 3; Page 32-33; 44pp; French.
XX
XX      The amino acid sequence of the Fc(epsilon) CH2'-CH4' fragment covering
XX      amino acids 226-547. The DNA sequence was isolated from a human myeloma
XX      266BL CDNA library screened with a probe corresp. to the N-terminus of
XX      Ige. The region encoding amino acids 218-547 was cloned into the vector

```

CC pwr211 under control of the tryptophan promoter. The resultant protein
 CC produced contains some non-Fc amino acids. These were removed by
 CC replacing their coding sequence with a bicistronic linker. The resultant
 CC construct encodes the Fc(epsilon) constant heavy region from amino acids
 CC 226-547. When it is expressed in E.coli, the protein produced is a
 CC non-glycosylated Fc(epsilon) fragment. Altering the pattern of
 CC glycosylation unmasks new antigenic sites thus rendering the Fc fragment
 CC immunogenic and able to induce antibodies that recognise native IgE but
 CC do not form histamine-releasing complexes. The Fc fragments can be used
 CC in anti-allergic vaccines to modulate the intensity of immune responses
 CC mediated by IgE.

XX Sequence 324 AA;

Query Match 100.0%; Score 1707; DB 16; Length 324;

Best Local Similarity 100.0%; Pred. No. 1,1e-129;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCGGHHFPTIOLCLVSGYPTGTINITWLEDQVMDVLDLSTASTQ 60
 DB 5 FTPTVKILQSSCGGHHFPTIOLCLVSGYPTGTINITWLEDQVMDVLDLSTASTQ 64
 QY 61 GELASTOSELTLSSQKHWLSDRTYTCQVYOGHTEFEDSTKCCADSNPRGVSAYLSRPSFD 120
 DB 65 GELASTOSELTLSSQKHWLSDRTYTCQVYOGHTEFEDSTKCCADSNPRGVSAYLSRPSFD 124
 QY 121 LFIKSPITICLVVDLAPSKGTVNLTWASRSGKPVNHSRKEEQRNGTLTVSTLPVGT 180
 DB 125 LFIKSPITICLVVDLAPSKGTVNLTWASRSGKPVNHSRKEEQRNGTLTVSTLPVGT 184
 QY 181 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 240
 DB 185 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 244
 QY 241 NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLLEVTRAEMEQKDEFTICRAV 300
 DB 245 NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLLEVTRAEMEQKDEFTICRAV 304
 QY 301 HEAAPSQTVORAVSVNPGK 320
 DB 305 HEAAPSQTVORAVSVNPGK 324

RESULT 5

AAR75225 AAR75225 standard; Protein: 325 AA.

XX AAR75225;

XX 10-NOV-1995 (first entry)

DE Human IgE Fc chain (amino acids 224-547) mutant sequence.

XX IGE Fc fragment; antiallergic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 149 /label= Asn371

FT Misc-difference 172 /note= "glycosylation site"

FT Misc-difference 172 /label= Asn394

FT Misc-difference 1 /note= "glycosylation site"

FT Misc-difference 1 /label= Val224

FT Misc-difference 2 /note= "any AA or deletion"

FT Misc-difference 3 /note= "Ala, any other AA, or deletion"

FT Misc-difference 3 /label= Ser226

FT /note= "any AA or deletion"

FT Misc-difference 4 /label= Arg227
 FT /note= "any AA or deletion"
 FT Misc-difference 5 /label= Asp228
 FT /note= "any AA or deletion"

PN W09514779-A.

PD 01-JUN-1995.

XX 22-NOV-1994; 94WO-CB02561.

XX 22-NOV-1993; 93GB-0024013.

XX (THRE-) 31 RES EXPL LTD.

XX (CLT) CELLTECH THERAPEUTICS LTD.

PI Gould HJ, Owens RJ, Sutton BJ, Young RJ;

XX WPI: 1995-206936/27.

XX NPSDB: AA08/474.

PT Mutated glycosylated polypeptide(s) contg. parts of human IgE-Fc

XX useful to study and treat allergy.

XX Disclosure: Page 6; 55pp; English.

XX The sequence represents a mutant sequence of a human IgE-Fc.

XX chimeric amino acids 224-547, which is of sufficient length to bind

XX Fc-epsilon RI and/or Fc-epsilon RI IgE receptor sites on human

XX cells. The protein is useful in the study and treatment of

XX allergy.

XX Sequence 325 AA;

Query Match 100.0%; Score 1707; DB 16; Length 325;

Best Local Similarity 100.0%; Pred. No. 1,1e-129;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCGGHHFPTIOLCLVSGYPTGTINITWLEDQVMDVLDLSTASTQ 60
 DB 6 FTPTVKILQSSCGGHHFPTIOLCLVSGYPTGTINITWLEDQVMDVLDLSTASTQ 65
 QY 61 GELASTOSELTLSSQKHWLSDRTYTCQVYOGHTEFEDSTKCCADSNPRGVSAYLSRPSFD 120
 DB 66 GELASTOSELTLSSQKHWLSDRTYTCQVYOGHTEFEDSTKCCADSNPRGVSAYLSRPSFD 125
 QY 121 LFIKSPITICLVVDLAPSKGTVNLTWASRSGKPVNHSRKEEQRNGTLTVSTLPVGT 180
 DB 126 LFIKSPITICLVVDLAPSKGTVNLTWASRSGKPVNHSRKEEQRNGTLTVSTLPVGT 185
 QY 181 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 240
 DB 186 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 245
 QY 241 NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLLEVTRAEMEQKDEFTICRAV 300
 DB 246 NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLLEVTRAEMEQKDEFTICRAV 305
 QY 301 HEAAPSQTVORAVSVNPGK 320
 DB 306 HEAAPSQTVORAVSVNPGK 325

RESULT 6

AAR77241 AAR77241 standard; Protein: 325 AA.

XX AAR77241;

XX 10-NOV-1995 (first entry)

DE Human IGE Fc chain (amino acids 224-547) wild-type sequence.
XX IGE Fc fragment; antiallergic.
KM Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 149 /label= Asn371
FT Misc-difference 149 /note= "glycosylation site"
FT Misc-difference 172 /label= Asn394
FT /note= "glycosylation site"
FT
FT
PN WO9514779-A.
XX
XX 01-JUN-1995.
XX 22-NOV-1994; 94WO-GB02561.
XX 22-NOV-1993; 93GB-0024013.
XX (THRE-) 31 RES EXPL. LTD.
PA (CLIF) CELLTECH THERAPEUTICS LTD.
XX
PI Gould HJ, Owens RJ, Sutton BJ, Young RJ;
XX WPI: 1995-206936/27.
DR N-PSDB: AAO91170.
XX
PT Mutated glycosylated polypeptide(s) contg. parts of human IGE-Fc
PT useful to study and treat allergy.
PS
XX Disclosure: Page 35-36; 55pp; English.
XX
CC The sequence represents the wild-type sequence of a human IGE-Fc
CC chain (amino acids 224-547) which is of sufficient length to bind
CC Fc-epsilon RI and/or Fc-epsilon RI IGE receptor sites on human
CC cells. The sequence is preferably mutated (see AAR75225) to
CC represent a protein encoding a protein where Cys225 is mutated,
CC optionally together with Val224, Ser226 and Arg227. The protein
CC is useful in the study and treatment of allergy.
XX
SQ Sequence 325 AA:

Query Match 100.0%; Score 1707; DB 16; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.1e-129;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCDGGHPPPTIQLCLVSGYTPGTINTITWLEDQVMDVDLSTASTQE 60
DB 6 FTPTVKILQSSCDGGHPPPTIQLCLVSGYTPGTINTITWLEDQVMDVDLSTASTQE 65
QY 61 GELASTQSELTSQKHWLSDRTYTCQVYQGHTEFEDSTKCKADSNPRGSAVLSRSPD 120
DB 66 GELASTQSELTSQKHWLSDRTYTCQVYQGHTEFEDSTKCKADSNPRGSAVLSRSPD 125
QY 121 LFIKRSPTITCLVLDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLVTSSTLPVGT 180
DB 126 LFIKRSPTITCLVLDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLVTSSTLPVGT 185
QY 181 RDWIGETYYQCVRTHPLPRALMRSTTKSGPRAPEVYAFATPEMPGSRDKRTLACLIQ 240
DB 186 RDWIGETYYQCVRTHPLPRALMRSTTKSGPRAPEVYAFATPEMPGSRDKRTLACLIQ 245
QY 241 NFMEDISVQWLNHEVQLPDARHSTTOPRKTKGSGFEVFSRLLEVTRAEMEOKDEFICRAV 300
DB 246 NFMEDISVQWLNHEVQLPDARHSTTOPRKTKGSGFEVFSRLLEVTRAEMEOKDEFICRAV 305
QY 301 HEAASPSQTVQRAVSVNPGK 320
DB 306 HEAASPSQTVQRAVSVNPGK 325

RESULT 7
AAB03642
ID AAB03642 standard; protein; 331 AA.
XX
AC AAB03642;
XX
DT 22-NOV-2000 (first entry)
XX
DE Human IGE heavy chain constant regions 2, 3 and 4.
XX
XX Human; immunoglobulin E; IGE; vaccination; infection; allergy;
KM asthma; eczema; immunogenic peptide.
XX
OS Homo sapiens.
XX
PN WO200025722-A2.
XX
XX 11-MAY-2000.
XX
XX 21-OCT-1999; 99WO-SE01896.
XX
XX 02-NOV-1998; 98US-0106652.
XX 22-SEP-1999; 99US-0401636.
XX (RESI-) RESISTENTIA PHARM AB.
XX
PI Hellman LT.
XX
XX WPI: 2000-365342/31.
DR
XX
XX Immunogenic polypeptides useful for preventing the harmful effects of
PT immunoglobulin E in mammals -
XX
PS Disclosure: Fig 1; 50pp; English.
XX
CC The present sequence is an immunogenic peptide consisting of the
CC heavy chain constant regions 2, 3 and 4 of the human IGE. It was used to
CC construct a number of immunogenic peptides which consisted of regions of
CC IGE from different mammals, which appear to cause a stronger polyclonal
CC anti-self IGE response than peptides consisting of the same regions from
CC one mammal. Immunogenic peptides, particularly those consisting of
CC different heavy chain constant regions, can be used for vaccination
CC in humans, against bacterial and viral infections and allergies, such
CC as asthma, fur, pollen and food allergies and eczema.
XX
SQ Sequence 331 AA:

Query Match 100.0%; Score 1707; DB 21; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.1e-129;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCDGGHPPPTIQLCLVSGYTPGTINTITWLEDQVMDVDLSTASTQE 60
DB 12 FTPTVKILQSSCDGGHPPPTIQLCLVSGYTPGTINTITWLEDQVMDVDLSTASTQE 71
QY 61 GELASTQSELTSQKHWLSDRTYTCQVYQGHTEFEDSTKCKADSNPRGSAVLSRSPD 120
DB 72 GELASTQSELTSQKHWLSDRTYTCQVYQGHTEFEDSTKCKADSNPRGSAVLSRSPD 131
QY 121 LFIKRSPTITCLVLDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLVTSSTLPVGT 180
DB 126 LFIKRSPTITCLVLDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLVTSSTLPVGT 185
QY 181 RDWIGETYYQCVRTHPLPRALMRSTTKSGPRAPEVYAFATPEMPGSRDKRTLACLIQ 240
DB 186 RDWIGETYYQCVRTHPLPRALMRSTTKSGPRAPEVYAFATPEMPGSRDKRTLACLIQ 251
QY 241 NFMEDISVQWLNHEVQLPDARHSTTOPRKTKGSGFEVFSRLLEVTRAEMEOKDEFICRAV 300
DB 252 NFMEDISVQWLNHEVQLPDARHSTTOPRKTKGSGFEVFSRLLEVTRAEMEOKDEFICRAV 311
QY 301 HEAASPSQTVQRAVSVNPGK 320

| Db | 312 | HEAASPSQTVORAVSVNPGK | 331 |
|---|---------------------------------------|----------------------|-----|
| RESULT 8 | | | |
| AA080291 | | | |
| AA080291 | standard; protein; 367 AA. | | |
| AA080291; | | | |
| 06-DEC-1990 | (first entry) | | |
| Interleukin-2/IgE Fc fusion protein. | | | |
| Interleukin-2; IgE Fc receptor; fusion protein; asthma; dermatitis. | | | |
| synthetic. | | | |
| Key | Location/Qualifiers | | |
| Peptide | 1..20 | | |
| Peptide | /label-IL-2 leader sequence | | |
| Peptide | 21..31 | | |
| Peptide | /label-IL-2 N-terminal | | |
| Peptide | 32..36 | | |
| Peptide | /label-linker | | |
| Peptide | 37..367. | | |
| EP269455-A. | | | |
| 01-JUN-1988. | | | |
| 27-NOV-1987; | 87EP-0310475. | | |
| 18-SEP-1987; | 87JP-0232295. | | |
| 28-NOV-1986; | 86JP-0281871. | | |
| (TAKE) TAKEDA CHEMICAL IND KK. | | | |
| Ikeyama S, Nishimura O; | | | |
| WPI; 1988-149211/22. | | | |
| Fused protein for allergy treatment - comprising interleukin-2 | | | |
| N-terminal residues, a linker and human immunoglobulin E Fc | | | |
| fragment. | | | |
| Disclosure; ; P; English. | | | |
| This fusion protein has a low toxicity and is useful in therapy | | | |
| for allergy induced by IgE. It can be used in the treatment of | | | |
| allergic dermatosis, atopic dermatitis or bronchial asthma. | | | |
| Sequence 367 AA; | | | |
| Query Match | 100.0%; Score 1707; DB 9; Length 367; | | |
| Best Local Similarity | 100.0%; Pred. No. 1.3e-129; | | |
| Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | |
| 1 FTPTVAVILKSSCGGGHFPPTIQLCLVSGYTGTTNITMLEGQVMDVLDSTASTQ | 60 | | |
| 48 FTPTVAVILKSSCGGGHFPPTIQLCLVSGYTGTTNITMLEGQVMDVLDSTASTQ | 107 | | |
| 61 GELASTQSEILSKQHWLSDRTYTCQVYQGTFEDSTKCADSNPRGSAVLSRPSFD | 120 | | |
| 108 GELASTQSEILSKQHWLSDRTYTCQVYQGTFEDSTKCADSNPRGSAVLSRPSFD | 167 | | |
| 121 LFIKRSPTITCLVVDLAPSKGTVALTWSRASGKPVNHSSTRKEKORNGTLTFTL | 180 | | |
| 168 LFIKRSPTITCLVVDLAPSKGTVALTWSRASGKPVNHSSTRKEKORNGTLTFTL | 227 | | |
| 181 RDMLEGEYQOCRVTHPHLPALMLNSTKTSQPPRAPEYATAPMPGSRKRTIACLIQ | 240 | | |
| 228 RDMLEGEYQOCRVTHPHLPALMLNSTKTSQPPRAPEYATAPMPGSRKRTIACLIQ | 287 | | |

| | | | | |
|----------|---|--|--|------|
| OY | | 241 | NFMEPEISVQWLNHEVQLPDARHSTTORPKTSGSEFPVESRLEYTPRAEMEKDEICTRAV | 3008 |
| | | | | |
| Db | | 288 | NFMEPEISVQWLNHEVQLPDARHSTTORPKTKGSEFPVSRLLEYTPRAEMEKDEICTRAV | 3477 |
| | | | | |
| OY | | 301 | HEAASPSQTIVORAVSYNPGK | 320 |
| | | | | |
| Db | | 348 | HEAASPSQTIVORAVSYNPGK | 367 |
| | | | | |
| RESULT 9 | | | | |
| ID | AAU80283 | standard; Protein: 428 AA. | | |
| XX | AAU80283: | | | |
| AC | | | | |
| XX | | | | |
| DT | 30-JUL-2002 | (first entry) | | |
| XX | | | | |
| DE | | | | |
| XX | | | | |
| KM | Human IGE heavy chain C1-C2-C3-C4 domains. | | | |
| KW | IGE: allergy; human; antiallergic; immunosuppressive; antiaphyllactic; | | | |
| KW | antisthmatic; dermatological; antiinflammatory; immunoglobulin E; IGE; | | | |
| KW | vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis; | | | |
| KW | heavy chain C domain. | | | |
| XX | | | | |
| OS | Homo sapiens. | | | |
| XX | | | | |
| Key | Location/Qualifiers | | | |
| FH | 11..116 | "IGE heavy chain C1 domain" | | |
| FT | /note= | | | |
| FT | 113..208 | "IGE heavy chain C2 domain" | | |
| FT | /label= | | | |
| FT | 205..219 | "Epitope including CZC3 linker" | | |
| FT | /note= | | | |
| FT | 209..216 | "Linker domain between C2 and C3 region" | | |
| FT | /note= | | | |
| FT | 217..316 | "IGE heavy chain C3 domain" | | |
| FT | /note= | | | |
| FT | 244..251 | "Epitope in BC loop" | | |
| FT | /note= | | | |
| FT | 244..251 | "Epitope in BC loop" | | |
| FT | /note= | | | |
| FT | 272..280 | "Epitope in DE loop" | | |
| FT | /note= | | | |
| FT | 301..311 | "Epitope in FG loop" | | |
| FT | /note= | | | |
| FT | 315..323 | "Epitope including C3C4 linker" | | |
| FT | /note= | | | |
| FT | 317..320 | "Linker between domains C3`andC4" | | |
| FT | /note= | | | |
| FT | 321..422 | "IGE heavy chain C4 domain" | | |
| FT | /note= | | | |
| PX | NO200220038-A2. | | | |
| XX | | | | |
| PD | 14-MAR-2002. | | | |
| XX | | | | |
| PF | 06-SEP-2001; 2001WO-DK00579. | | | |
| XX | | | | |
| PR | 06-SEP-2000; 2000DK-0001326. | | | |
| PR | 15-SEP-2000; 2000US-232831P. | | | |
| XX | | | | |
| PA | (PHAR-) PHAREXA AS. | | | |
| XX | | | | |
| PI | Klysner S, Von Hoegen P, Voldborg B, Gautam A; | | | |
| DR | WPT; 2002-383033/41. | | | |
| XX | | | | |
| PT | Including immune response against autologous immunoglobulin E in an | | | |
| PT | animal, by effecting simultaneous presentation of cytotoxic T | | | |
| PT | lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin | | | |
| XX | | | | |

PS Examples; Page 101-103; 151pp; English.

This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful for the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C1-C2-C3-C4 domains used to create the epitopes of the invention.

SQ Sequence 428 AA;

| | | | | |
|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match | 100.0%; | Score 1707; | DB 23; | Length 428; |
| Best Local Similarity | 100.0%; | Pred. No. 1.5e-129; | | |
| Matches 320; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|--|-----|
| QY | 1 | FFPPYKLIQSSCDGGHPPIITQLCLVSGTGTINITLDEGQVMDVLSNSTOE | 60 |
| Db | 109 | FFPPYKLIQSSCDGGHPPIITQLCLVSGTGTINITLDEGQVMDVLSNSTOE | 168 |
| QY | 61 | GELASTQSELTLQKHWLSDRTTYTCQVYTCQGHTEPDSKTCADSNPGVASYLSRPSFD | 120 |
| Db | 169 | GELASTQSELTLQKHWLSDRTTYTCQVYTCQGHTEPDSKTCADSNPGVASYLSRPSFD | 228 |
| QY | 121 | LFIKRSPTITCLVVDLAPSKGTVNLTWMSRASKPVNHSTRKEEKORNGTLVYVSTLPGVT | 180 |
| Db | 229 | LFIKRSPTITCLVVDLAPSKGTVNLTWMSRASKPVNHSTRKEEKORNGTLVYVSTLPGVT | 288 |
| QY | 181 | RDMISETTYQCRTVHPHLPALMRSTYTSQGPRAPEVYAFATPEMFGSRDKRTLACLIO | 240 |
| Db | 289 | RDMISETTYQCRTVHPHLPALMRSTYTSQGPRAPEVYAFATPEMFGSRDKRTLACLIO | 348 |
| QY | 241 | NFMPEDISYQWLHNEQVLPDARHSTYQPRKTKGSGFEFYSRLVETYARAMEBKDEIFICRAV | 300 |
| Db | 349 | NFMPEDISYQWLHNEQVLPDARHSTYQPRKTKGSGFEFYSRLVETYARAMEBKDEIFICRAV | 408 |
| QY | 301 | HEAASPQTVQRAVSYNPKG | 320 |
| Db | 409 | HEAASPQTVQRAVSYNPKG | 428 |

RESULT 10
AAM50940

AC AAM50940;

DT 15-MAY-2002 (first entry)

DE Human Ige epsilon chain constant region.

KW iGE; immunoglobulin E; antibody; human; allergy; asthma; eczema;
KW urticaria; anaphylactic shock; allergic rhinitis; conjunctivitis;
KW antianaphylactic; immunosuppressive; antiallergic; antisthmatic;
KW antiinflammatory; dermatological; vasotropic; ophthalmological;
KW vaccine; therapy.

OS Homo sapiens.

| FH | Key | Location/Qualifiers |
|-----|-----|---------------------|
| 1 | 1 | 1 |
| 2 | 2 | 2 |
| 3 | 3 | 3 |
| 4 | 4 | 4 |
| 5 | 5 | 5 |
| 6 | 6 | 6 |
| 7 | 7 | 7 |
| 8 | 8 | 8 |
| 9 | 9 | 9 |
| 10 | 10 | 10 |
| 11 | 11 | 11 |
| 12 | 12 | 12 |
| 13 | 13 | 13 |
| 14 | 14 | 14 |
| 15 | 15 | 15 |
| 16 | 16 | 16 |
| 17 | 17 | 17 |
| 18 | 18 | 18 |
| 19 | 19 | 19 |
| 20 | 20 | 20 |
| 21 | 21 | 21 |
| 22 | 22 | 22 |
| 23 | 23 | 23 |
| 24 | 24 | 24 |
| 25 | 25 | 25 |
| 26 | 26 | 26 |
| 27 | 27 | 27 |
| 28 | 28 | 28 |
| 29 | 29 | 29 |
| 30 | 30 | 30 |
| 31 | 31 | 31 |
| 32 | 32 | 32 |
| 33 | 33 | 33 |
| 34 | 34 | 34 |
| 35 | 35 | 35 |
| 36 | 36 | 36 |
| 37 | 37 | 37 |
| 38 | 38 | 38 |
| 39 | 39 | 39 |
| 40 | 40 | 40 |
| 41 | 41 | 41 |
| 42 | 42 | 42 |
| 43 | 43 | 43 |
| 44 | 44 | 44 |
| 45 | 45 | 45 |
| 46 | 46 | 46 |
| 47 | 47 | 47 |
| 48 | 48 | 48 |
| 49 | 49 | 49 |
| 50 | 50 | 50 |
| 51 | 51 | 51 |
| 52 | 52 | 52 |
| 53 | 53 | 53 |
| 54 | 54 | 54 |
| 55 | 55 | 55 |
| 56 | 56 | 56 |
| 57 | 57 | 57 |
| 58 | 58 | 58 |
| 59 | 59 | 59 |
| 60 | 60 | 60 |
| 61 | 61 | 61 |
| 62 | 62 | 62 |
| 63 | 63 | 63 |
| 64 | 64 | 64 |
| 65 | 65 | 65 |
| 66 | 66 | 66 |
| 67 | 67 | 67 |
| 68 | 68 | 68 |
| 69 | 69 | 69 |
| 70 | 70 | 70 |
| 71 | 71 | 71 |
| 72 | 72 | 72 |
| 73 | 73 | 73 |
| 74 | 74 | 74 |
| 75 | 75 | 75 |
| 76 | 76 | 76 |
| 77 | 77 | 77 |
| 78 | 78 | 78 |
| 79 | 79 | 79 |
| 80 | 80 | 80 |
| 81 | 81 | 81 |
| 82 | 82 | 82 |
| 83 | 83 | 83 |
| 84 | 84 | 84 |
| 85 | 85 | 85 |
| 86 | 86 | 86 |
| 87 | 87 | 87 |
| 88 | 88 | 88 |
| 89 | 89 | 89 |
| 90 | 90 | 90 |
| 91 | 91 | 91 |
| 92 | 92 | 92 |
| 93 | 93 | 93 |
| 94 | 94 | 94 |
| 95 | 95 | 95 |
| 96 | 96 | 96 |
| 97 | 97 | 97 |
| 98 | 98 | 98 |
| 99 | 99 | 99 |
| 100 | 100 | 100 |

FT Domain

13

| | |
|--------|-------------|
| Domain | 313..428 |
| FT | /label= CH4 |
| FT | |

PN W0200209751-A2

XX 07-FEB-2002
PD

PF 23-JUL-2001; 2001WO-IB01353

PR 28-JUL-2000; 2000US-221841P

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PA (RENN/) RENNER W A.

PI Bachmann MF, Renner WA;

DR WPI; 2002-227076/28.

Composition for treatment

PT Composition for treating immunoglobulin (Ig) E-mediated disorder such
PT as anaphylactic shock, allergic rhinitis and conjunctivitis, comprises
PT a polypeptide that includes CH1 and/or CH4 domains of IgE molecule
PT coupled to a carrier -

PS Claim 41; Page 9; 71pp; English.

The present sequence is that of the human IGE epsilon chain constant region. The invention is based on the discovery that a polypeptide that includes the CH1 (i.e. constant domain 1 in the heavy chain) and/or CH4 domain(s) of an IGE molecule, coupled to a carrier, can be used to induce in a mammal the production of antibodies that specifically bind to IGE of the mammal. Compositions are provided for inducing self-specific anti-IGE antibodies. These contain carriers foreign to the immunised mammal coupled to polypeptides containing fragments of the IGE molecule, especially fragments including the constant CH1 and/or CH4 domain, but not the CH3 domain. CH1 polypeptides have at least 95% identity to amino acids 1-110, 105, 5-105 or 5-95 of the present sequence, while CH4 polypeptides have at least 95% identity to amino acids 313-428, 313-425, 317-428 or 317-425 of the present sequence. The anti-IGE antibodies reduce or eliminate the pool of free IGE in the mammal's serum. Alternatively, a polynucleotide encoding a fusion protein comprising the carrier and IGE-derived polypeptide is administered. The compositions and polynucleotides are used to inhibit or treat IGE-mediated disorders such as anaphylactic shock, allergic rhinitis or conjunctivitis, an allergic reaction to an allergen such as fur, dust or food, an asthmatic reaction, eczema or urticaria (all claimed).

SQ Sequence 428 AA;

| | | | | |
|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match | 100.0%; | Score 1707; | DB 23; | Length 428; |
| Best Local Similarity | 100.0%; | Pred. No. 1.5e-129; | | |
| Matches 320; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

```

QY      1  FFFPPYKLISSODGGGHPPTIOLLCVSGTGTINIMLEGGQVMDVLSSTAHTOE 60
Db      109  FFFPPYKLISSODGGGHPPTIOLLCVSGTGTINIMLEGGQVMDVLSSTAHTOE 168
QY      61  GELASTQSELTLSOKHMLSDRYTCQVTVYOGHTEEDSTKKCADSNPRGVSAYLSRSPFD 120
Db      169  GELASTQSELTLSOKHMLSDRYTCQVTVYOGHTEEDSTKKCADSNPRGVSAYLSRSPFD 228
QY      121  LFRKSPPTITCLVNDLAPSKGTVNLTWMSRASKPVNHSFRKEEKORNGTLTVSTLPEVT 180
Db      229  LFRKSPPTITCLVNDLAPSKGTVNLTWMSRASKPVNHSFRKEEKORNGTLTVSTLPEVT 288
QY      181  RDMIEBETVQCRNTHHPLRALMRSTYTTSGRRAPPEYAAATATEWMSGSDKRTKLACLIQ 240
Db      289  RDMIEBETVQCRNTHHPLRALMRSTYTTSGRRAPPEYAAATATEWMSGSDKRTKLACLIQ 348
QY      241  NFMEPEISVQWMLHNEVQLPDARHSTTORPKTKGSGFEFYSRLEVTARAMEBOKDEFCICRAV 300
Db      349  NFMEPEISVQWMLHNEVQLPDARHSTTORPKTKGSGFEFYSRLEVTARAMEBOKDEFCICRAV 408
QY      301  HEASPSQTVQRAVSYNPGK 320

```


CC acid sequences used in the exemplification of the present invention.
 XX Sequence 325 AA:

Query Match 99.6%; Score 1701; DB 21; Length 325;
 Best Local Similarity 99.4%; Pred. No. 3.3e-129;
 Matches 318; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTPVKILQSSCDGGHPPPTIOLCLVSGYTPGTINTITWLEDQVMDVDLSTASTQ 60
 |||
 DB 6 FTPTPVKILQSSCDGGHPPPTIOLCLVSGYTPGTINTITWLEDQVMDVDLSTASTQ 65
 QY 61 GELASTQSELTLSQKHWLSDRTTYTCQVYTGHTFEDSTKCKADSNPRGSAVLSRSPD 120
 |||
 DB 66 GELASTQSELTLSQKHWLSDRTTYTCQVYTGHTFEDSTKCKADSNPRGSAVLSRSPD 125
 QY 121 LFIKRSPTITCLVVDLAPSKGTVNLTWASRASKPVNHSTRKEKORNGTLVTSLLPVGT 180
 |||
 DB 126 LFIKRSPTITCLVVDLAPSKGTVNLTWASRASKPVNHSTRKEKORNGTLVTSLLPVGT 185
 QY 181 RDMWIGETTYQCRVTHPHLPALMRSTTKTSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 240
 |||
 DB 186 RDMWIGETTYQCRVTHPHLPALMRSTTKTSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 245
 QY 241 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTKSGEFVSRLEVTARAWEQKDEFICRAV 300
 |||
 DB 246 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTKSGEFVSRLEVTARAWEQKDEFICRAV 305
 QY 301 HEAASPSQTVQRAVSNP 320
 |||
 DB 306 HEAASPSQTVQRAVSNP 325

RESULT 13

AAU80288
 ID AAU80288 standard; Protein; 336 AA.

AC AAU80288;

DT 30-JUL-2002 (first entry)

DE Human IGE heavy chain C2-C3-C4 domains with MIGIS fragment.

XX IGE; allergy; human; antiallergic; immunosuppressive; anti-anaphylactic;
 KW antilastmatic; dermatological; anti-inflammatory; immunoglobulin E; IGE;
 KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
 KW heavy chain C domain; MIGIS.

OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

FT 8..103 /note="IGE heavy chain C2 domain"
 FT 100..114 /note="Epitope including C2C3 linker"
 FT 104..111 /note="Linker domain between C2 and C3 region"
 FT 112..211 /note="IGE heavy chain C3 domain"
 FT 139..145 /note="Epitope in BC loop"
 FT 167..175 /note="Epitope in DE loop"
 FT 196..206 /note="Epitope in FG loop"
 FT 210..218 /note="Epitope including C3C4 linker"
 FT 212..215 /note="Linker between domains C3 and C4"
 FT 216..317 /note="IGE heavy chain C4 domain"
 FT 217..317

FT /note="IGE heavy chain C3 domain"
 FT 322..336 /note="MIGIS fragment"

PN WO200220038-A2.

PD 14-MAR-2002.

PF 06-SEP-2001; 2001WO-DK00579.

PR 06-SEP-2000; 2000DK-0001326.

PR 15-SEP-2000; 2000US-232831P.

PA (PHAR-) PHARMEXA AS.

PI Klynsner S, Von Hoegen P, Voldborg B, Gautam A;

DR WPI; 2002-383033/41.

PT Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin

PS Examples; Page 116-117; 151pp; English.

This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IGE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IGE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IGE in an animal, which is useful for downregulating CC autologous IGE in the animal. This method is useful in the prevention CC and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents CC the human IGE heavy chain C2-C3-C4 domains fused to the MIGIS CC fragment used to create the epitopes of the invention.

XX Sequence 336 AA:

Query Match 99.4%; Score 1696; DB 23; Length 336;

Best Local Similarity 100.0%; Pred. No. 8.6e-129;

Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTPVKILQSSCDGGHPPPTIOLCLVSGYTPGTINTITWLEDQVMDVDLSTASTQ 60
 |||
 DB 4 FTPTPVKILQSSCDGGHPPPTIOLCLVSGYTPGTINTITWLEDQVMDVDLSTASTQ 63
 QY 61 GELASTQSELTLSQKHWLSDRTTYTCQVYTGHTFEDSTKCKADSNPRGSAVLSRSPD 120
 |||
 DB 64 GELASTQSELTLSQKHWLSDRTTYTCQVYTGHTFEDSTKCKADSNPRGSAVLSRSPD 123
 QY 121 LFIKRSPTITCLVVDLAPSKGTVNLTWASRASKPVNHSTRKEKORNGTLVTSLLPVGT 180
 |||
 DB 124 LFIKRSPTITCLVVDLAPSKGTVNLTWASRASKPVNHSTRKEKORNGTLVTSLLPVGT 183
 QY 181 RDMWIGETTYQCRVTHPHLPALMRSTTKTSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 240
 |||
 DB 184 RDMWIGETTYQCRVTHPHLPALMRSTTKTSGPRAPEVYAFATPEWPGSRDKRTIACLIQ 243
 QY 241 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTKSGEFVSRLEVTARAWEQKDEFICRAV 300
 |||
 DB 244 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTKSGEFVSRLEVTARAWEQKDEFICRAV 303
 QY 301 HEAASPSQTVQRAVSNP 318
 |||
 DB 304 HEAASPSQTVQRAVSNP 321

RESULT 14

AAU80287
 ID AAU80287 standard; Protein: 441 AA.
 XX
 AC AAU80287;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Human IGE heavy chain C1-C2-C3-C4 domains with MIGIS fragment.
 XX
 KW IGE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
 KW antiaesthetic; dermatological; antiinflammatory; immunoglobulin E; IGE;
 KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
 KW heavy chain C domain; MIGIS.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FT Key location/Qualifiers
 FT Domain 11..106
 FT /note= "IGE heavy chain C1 domain"
 FT 113..208
 FT /label= IGE heavy chain C2 domain
 FT 205..219
 FT /note= "Epitope including C2C3 linker"
 FT Region 209..216
 FT /note= "Linker domain between C2 and C3 region"
 FT 217..317
 FT /note= "IGE heavy chain C3 domain"
 FT 244..251
 FT /note= "Epitope in BC loop"
 FT 244..251
 FT /note= "Epitope in BC loop"
 FT Region 272..280
 FT /note= "Epitope in DE loop"
 FT 301..311
 FT /note= "Epitope in FG loop"
 FT Region 315..323
 FT /note= "Epitope including C3C4 linker"
 FT Region 318..320
 FT /note= "Linker between domains C3 and C4"
 FT 321..422
 FT /note= "IGE heavy chain C4 domain"
 FT 427..421
 FT /note= "MIGIS fragment"
 FT Domain
 XX
 PN MO200220038-A2.
 XX
 XX 14-MAR-2002.
 PD
 XX
 PF 06-SEP-2001; 2001WO-DK00579.
 XX
 XX 06-SEP-2000; 2000DK-0001326.
 PR 15-SEP-2000; 2000US-232831P.
 XX
 XX (PHAR-) PHARMAXA AS.
 PA
 XX
 PI Klysner S, Von Hoegen P, Voldborg B, Gautam A;
 XX
 DR WPI: 2002-383033/41.
 XX
 XX
 PT Inducing immune response against autologous immunoglobulin E in an
 PT animal, by effecting simultaneous presentation of cytotoxic T
 PT lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
 PT
 XX
 XX Examples: Page 116-117; 151pp; English.
 PS
 XX
 CC This invention relates to a novel method for inducing an immune response
 CC against autologous immunoglobulin E (IGE) in an animal. The method
 CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
 CC (CTL) epitope and/or B-cell epitope derived from IGE, and T helper cell
 CC epitope (TH epitope) which is foreign to the animal, by antigen
 CC presenting cells (APCs) of the animal's immune system. The epitopes

CC of the invention may be used as a vaccine against allergic diseases. The
 CC method of the invention is useful for inducing an immune response
 CC against autologous IGE in an animal, which is useful for downregulating
 CC autologous IGE in the animal. This method is useful in the prevention
 CC and treatment of allergic diseases such as anaphylaxis, allergic
 CC rhinitis, asthma and atopic dermatitis. The present sequence represents
 CC the human IGE heavy chain C1-C2-C3-C4 domains fused to the MIGIS
 CC fragment used to create the epitopes of the invention.
 XX
 SQ Sequence 441 AA;
 Query Match 99.4%; Score 1696; DB 23; Length 441;
 Best Local Similarity 100.0%; Pred. No. 1.2e-128;
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTPTVKILQSSCDGGHFPPTIQLCLVSGTPTGTTINITWLEDGQVMDVLDLSTAQE 60
 DB 109 FTPTVKILQSSCDGGHFPPTIQLCLVSGTPTGTTINITWLEDGQVMDVLDLSTAQE 168
 QY 61 GELASTQSELTLSQKHWLSDRTTYTCQVYQGTEDSTKRCADSNPRGSAYLSRPSFD 120
 DB 169 GELASTQSELTLSQKHWLSDRTTYTCQVYQGTEDSTKRCADSNPRGSAYLSRPSFD 228
 QY 121 LFIKRSPTITCLVVDLAPSKGTVMLTWSRASKPVNHSRKEKORNGTLTVSTLPVGT 180
 DB 229 LFIKRSPTITCLVVDLAPSKGTVMLTWSRASKPVNHSRKEKORNGTLTVSTLPVGT 288
 QY 181 RDWIEGETYQCRVTHPHLPALMRSTTKSGPRAPEVYATPEWPSRDKRTIACLIQ 240
 DB 289 RDWIEGETYQCRVTHPHLPALMRSTTKSGPRAPEVYATPEWPSRDKRTIACLIQ 348
 QY 241 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTKSGGFVFSLEYTRAEMEKDEFICRAV 300
 DB 349 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTKSGGFVFSLEYTRAEMEKDEFICRAV 408
 QY 301 HEAASPSQTVORAVSNVP 318
 DB 409 HEAASPSQTVORAVSNVP 426
 RESULT 15
 AAP40065
 ID AAP40065 standard; Protein: 493 AA.
 AC AAP40065;
 XX
 XX 12-FEB-1992 (first entry)
 DT
 XX
 DE Sequence of human immunoglobulin E H-chain.
 XX
 KW Antibody; allergy suppressor; immunological.
 XX
 OS Homo sapiens.
 OS
 PN EP102634-A.
 XX
 PD 14-MAR-1984.
 XX
 PF 03-SEP-1983; 83EP-0108699.
 XX
 PR 07-SEP-1982; 82JP-0156285.
 XX
 PA (TAKE) TAKEDA CHEMICAL IND KK.
 XX
 PI Kikuchi M, Kurokawa T, Onda H;
 XX
 DR WPI: 1984-070437/12.
 DR N-PSDB: AAN40062.
 XX
 PT Polypeptide having activity of human immunoglobulin E - prepd.
 PT from host transformed with recombinant DNA
 XX
 PS Disclosure; Fig 2; 61pp; English.

XX DNA encoding Ige H-chain and frags. is claimed (AAN40062).
CC Transformant contg. the DNA is also new, esp. Escherichia coli IFO-
CC 14284, -5 and -6. The transformant may be grown to produce a
CC polypeptide of immunological or biological activity equivalent to
CC that of the human Ige H chain. AAN40062 or frags. is pref. linked at a
CC site downstream from a promoter, e.g. rec A promoter (see AAN40064).
XX

SQ Sequence 493 AA:

Query Match 99.2%; Score 1693; DB 5; Length 493;

Best Local Similarity 99.4%; Pred. No. 2.5e-128;

Matches 318; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | FTPTVKILQSSCDGSGHFPPTIOLCLVSGYTPGTINITWLEDQVMDVDLSTASTOE | 60 |
| | | | |
| DB | 174 | FTPTVKILQSSCDGSGHFPPTIOLCLVSGYTPGTINITWLEDQVMDVDLSTASTOE | 233 |
| | | | |
| QY | 61 | GELASTQSELTLISQKHWLSDRTYTCQVYQGHTEFEDSTKCCADSNPRGVSAVLSRPPD | 120 |
| | | | |
| DB | 234 | GELASTQSELTLISQKHWLSDRTYTCQVYQGHTEFEDSTKCCADSNPRGVSAVLSRPPD | 293 |
| | | | |
| QY | 121 | LFIRKSPITTCVVDLAPSKGVNLTWSRASGKPVNHSTRKEKORNGTLVTSILPVGT | 180 |
| | | | |
| DB | 294 | LFIRKSPITTCVVDLAPSKGVNLTWSRASGKPVNHSTRKEKORNGTLVTSILPVGT | 353 |
| | | | |
| QY | 181 | RDWIGETVOCRVTHPLPRALMRSTTKSGPRAPEVYAFATPEMPGSRDRTLACLIO | 240 |
| | | | |
| DB | 354 | RDWIGETVOCRVTHPLPRALMRSTTKSGPRAPEVYAFATPEMPGSRDRTLACLIO | 413 |
| | | | |
| QY | 241 | NMPEDISVQWLHNEVQLPDARHSTTOPRKTKGSGFVFSRLVTRAEMEQRDEFICRAV | 300 |
| | | | |
| DB | 414 | NMPEDISVQWLHNEVQLPDARHSTTOPRKTKGSGFVFSRLVTRAEMEQRDEFICRAV | 473 |
| | | | |
| QY | 301 | HEAASPSQTVQRAVSVNPGK | 320 |
| | | | |
| DB | 474 | HEAASPSQTVQRAVSVNPGK | 493 |
| | | | |

Search completed: July 15, 2003, 06:57:40
Job time : 39.6806 secs

Db 4 TAPKVFALAPGC--GTTSDSTVALGCLVSGYFEPPEVKVSW--NSGSLTSGVHTFSPVLQSS 60
QY 62 ELASTOSELTLSQKHMISDRITTCQVYVYQGHFF-----DSTKKCADSN--PR--- 107
Db 61 GFYSLSWVYVPASTWSE--TYICNVVAASNFVFKRIEPIPDNHQKVCMSKPCPA 119
QY 108 -----GVSAYLSRSPSPD-LFIRKSPITTCVLDLAPSKGVNLJWMSASAKPYNHNRK 161
Db 120 PELLGGFSPVFEPFPPNPKDTLITTRIPETVCVVDVSOENPDVKTNWYDGVETATTRP 179
QY 162 EKKRNGTLVATVSTLPGVTRDMIGETTYOCRVTHPHLPALMRSTTSGPRAAPEVYAF 221
Db 180 KEQGFNSTYRVVSLRIQHOMLWGSKFEKCKVNNQALPQIERITITTKRSGQEPQVYL 239
QY 222 ATPMPSSRDKRTIACLIONMPEDISVOMLHNEVOLDPARNHSTTOPRKTKGSGFFVFSR 281
Db 240 APHDELKSKSVSTYVCKVDEYPPPEINEMOSNGPPELETXYSTTQAOQSDSGSYFLYSK 299
QY 282 LEVTRAEMOEKDEFICRAVHEAASPSQTVORAVSVNGK 320
Db 300 LSVDRNRMOGCTTTCGVMEHALNHYT-QANVSKNPGK 337

RESULT 2

08VCX7 PRELIMINARY; PRT; 613 AA.
AC 08VCX7;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 67.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SALIVARY GLAND;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC018315, AA018315.1;
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF000409; Ig_2.
DR SMART: SM00409; Ig_2.
DR SMART: SM00407; IgC1; 4.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C2862 CRC64;

Query Match 25.2%; Score 430.5; DB 11; Length 613;
Best Local Similarity 32.3%; Pred. No. 1e-30;
Matches 104; Conservative 56; Mismatches 149; Indels 13; Gaps 8;

QY 4 PTYKIIQSSCDG-GGHPPTIQLCLVSGYTPGTINTMLEDGQVMDVLDASTAQEGE 62
Db 249 PNANVVEVPPRDGSGPAPRSKSLICEATNFTPKPIYMSKDKGLVSGFTTPVTELEK 308
QY 63 LASTQ-----SELTLSQKHMISDRITTCQVYVYQGHFF-EDSTKKCADSNRGVSAVLSRP 116
Db 309 GSTRPQYKIVSTLISIDMLNINVTYCRVDHGLFTLKNVSSSCAASPSDITITP 368
QY 117 SPDLFIRKSPITTCVLDLAPSKGVNLJWMSASAKPYNHNRK 176
Db 369 SFADIFLSKSNLTCVSNLATEY-FLNISWASQSGPLETKIKIMESHNGTFSAGVA 427
QY 177 PVGTROMIEGETYOCRVTHPHLPALMRSTTSGPRAAPEVYAFAP--EWGSRDKRT 234
Db 428 SVCVEEDMNNRKEVCVTHRLDPSPOKFKISKNEVHKHPAVAYLLPPAREOLNRESAT 487

QY 235 LACLIONMPEDISVOMLHNEVOLDPARNHSTTOPRKTKGSG-FFVTSRLVETRAEBOK 292
Db 488 VTCLVKGSPADISVOMLQRCQLPQEKYVTSAPMEPGAGFYFTSHILVTEEWNSG 547
QY 293 DEFICRAVHEAASPSQTVORAV 314
Db 548 EFTYCVGHEAL-PLYTERIV 568

RESULT 3

08R3V9 PRELIMINARY; PRT; 469 AA.
AC 08R3V9;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC024405; AA024405.1;
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51976 MW; 534793F15D05457 CRC64;

Query Match 24.3%; Score 414; DB 11; Length 469;
Best Local Similarity 29.5%; Pred. No. 2.3e-29;
Matches 97; Conservative 60; Mismatches 154; Indels 18; Gaps 7;

QY 2 TPPTVKIIQSSCDGCGHPPPTIQLCLVSGYTPGTINTMLEDGQVMDVLDASTAQEG 61
Db 149 TPPEVYPLAPG--SAAQTNSMVTGLCLVKGFEPPVITW--NSGSLSGVHTFPAVLQSS 204
QY 62 ELASTOSELTLSQKHMISDRITTCQVYVYQGHFF-----DSTKKCADSNRGVSAV 112
Db 205 DLYLSSSVTPSPSTWS-OTVTCNVANHPASSSTKVDKRIIPRDGCKPCICTVPEVSSVF 263
QY 113 LSRSPPD-LFIRKSPITTCVLDLAPSKGVNLJWMSASAKPYNHSTREKORNGTLT 171
Db 264 IPPPKRPDVLITLITPRKVTCCVVDISKDDPEVQSWVDDVENVTAOTKREDFNSTFR 323
QY 172 VTSTLPVGTDMIEGETYOCRVTHPHLPALMRSTTSGPRAAPEVYAFATPEWPGSRD 231
Db 324 SVSELPIMHODWLNKGEKFCRVNSAAPPAPIEKTISKGRPKAPQVYITIPPEQMAKD 383
QY 232 KRTIACLIONMPEDISVOMLHNEVOLDPARNHSTTOPRKTKGSGFFVTSRLVETRAEBOK 291
Db 384 KVSILTCMTDFFPEDITVEMOWN--GPAENYKNTOPIMDTSYFYSKLNVOKSMWEA 441
QY 292 KDEFCRAVHEAASPSQTVORAVSVNGK 320
Db 442 GNETFCVLEHGLNHHHT-EKSLSHSPCK 469

RESULT 4

09BSZ1 PRELIMINARY; PRT; 375 AA.
AC 09BSZ1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Hypothetical 41.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH;

| Query | Database | Score | DB | Length | Mismatches | Indels | Gaps |
|----------|--|-------|-----|--------|------------|--------|------|
| QY | 3 PPTVKILISCGDGGHPPTIQLLGSYTPGTITNTLWLEDQVMDYDLSTASTTQGE | 24.2% | 413 | 375 | 62 | 12 | 8 |
| Db | Best Local Similarity 28.7%, Pred. No. 2, 1e-29. | | | | | | |
| Matches | 94, Conservative 63, Mismatches 159, Indels 12, Gaps 8 | | | | | | |
| QY | 63 LA-----STGSELLISQKHMLSDRTYTCQVYVYQGHTF-EDSTKCKADSNPKGVSAVYLSRP | | | | | | |
| Db | 92 ESGPTTKYKVTSTLTIKESDMLISQSMFTCRVHRRGLTFQOANSSMCVPPDDTAIRVFAIRP | | | | | | |
| QY | 117 SPPELFIKRSPTITICLVNDLAPSKGVALTWMSRAGKRVNNSSTKREKORNGTLTVTSTL | | | | | | |
| Db | 152 SFASIFLTKSKTKLCIVLVDL-ITDVSATISMTROGKENVKTHNTISESHPNATFSAVGEA | | | | | | |
| QY | 177 PVGRDWMIEGTYOCRTVTHPHLPRLALMRSTTKTSGPRA-ADPVYAF-ATPEWGSRDRT | | | | | | |
| Db | 211 SICEDDWNMSGRFTCTVYHTDLPSPKOTISRPKGVALLHRDVTLLPAREQLNRESAT | | | | | | |
| QY | 235 LACIIONMPEDISOYOMLHNEVOLDPAHSTTOPR-KTKGSG-FFVESRLFTTBAEWGQ | | | | | | |
| Db | 271 ITCIVTGSPADVYQWNRQOPLSPKRYVTSAPRPEQAFGRYAHSLIYSEEWNTG | | | | | | |
| QY | 293 DEFCRAVHEAASPSQTVQRAVSVNPGK | | | | | | |
| Db | 331 ETVTCVVAHEAL-PNRKVTERTVDKSTGK | | | | | | |
| RESULT 5 | | | | | | | |
| Q99LC4 | PRELIMINARY; | PRT; | 463 | AA. | | | |
| AC | 099LC4; | | | | | | |
| DT | 01-JUN-2001 (TREMBLrel. 17, Created) | | | | | | |
| DT | 01-JUN-2001 (TREMBLrel. 17, Last sequence update) | | | | | | |
| DT | 01-JUN-2002 (TREMBLrel. 21, Last annotation update) | | | | | | |
| DE | Similar to RIKEN CDNA 1810060009 gene. | | | | | | |
| GN | IGH-4. | | | | | | |
| OS | Mus musculus (Mouse). | | | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | | |
| CC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | | | |
| OX | NCBI_TaxID=10090; | | | | | | |
| RN | [1] | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | |
| RA | Strausberg R.; | | | | | | |
| RL | Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases. | | | | | | |
| DR | EMBL; BC000435; AA03435.1; - | | | | | | |
| DR | HSSP; P01842; 7FAB. | | | | | | |
| DR | MGP; MGI:96446; Igh-4. | | | | | | |
| DR | InterPro; IPR003599; Ig. | | | | | | |
| DR | InterPro; IPR003597; Ig_c1. | | | | | | |
| DR | InterPro; IPR003600; Ig_like. | | | | | | |
| DR | InterPro; IPR003006; Ig_MHC. | | | | | | |
| DR | InterPro; IPR003596; Ig_v. | | | | | | |
| DR | Pfam; PF00047; Ig: 4. | | | | | | |
| DR | SMART; SM00409; Ig: 2. | | | | | | |
| DR | SMART; SM00407; IGL1.2. | | | | | | |
| DR | SMART; SM00406; IGV.1. | | | | | | |
| DR | SMART; SM00410; IG_like.1. | | | | | | |

[illegible]

| | | | |
|-----------------------|---|--------------------|-----------------------------------|
| RESULT 6 | | | |
| 09BOB8 | PRELIMINARY: | PRT: | 597 AA. |
| ID | 09BOB8 | | |
| AC | 09BOB8; | | |
| DT | 01-JUN-2001 (TRENBLREL. 17, Created) | | |
| DT | 01-JUN-2001 (TRENBLREL. 17, Last sequence update) | | |
| DT | 01-DEC-2001 (TRENBLREL. 19, Last annotation update) | | |
| DE | Unknown (protein for MGC:1905) (protein for MGC:1128). | | |
| OS | Homo sapiens (Human) | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| NCBI_TaxId | 9606; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | TISSUE=MUSCLE; | | |
| RA | Strausberg R.; | | |
| RL | Submitted (APR-2001) to the EMBL/GenBank/DBJ databases. | | |
| RN | [2] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | TISSUE=LYMPH; | | |
| RA | Strausberg R.; | | |
| RL | Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases. | | |
| DR | EMBL; BC006180; AAH06180.1; - | | |
| DR | EMBL; BC001872; AAH01872.1; - | | |
| DR | HSSP; P01825; 7FAB. | | |
| DR | InterPro; IPR003599; I9 | | |
| DR | InterPro; IPR003597; I9_CL | | |
| DR | InterPro; IPR003600; I9_ILKE | | |
| DR | InterPro; IPR003006; I9_MHC | | |
| DR | InterPro; IPR003596; I9_V | | |
| DR | Pfam; PF00047; I4; 5 | | |
| DR | SMART; SM00409; IG; 2 | | |
| DR | SMART; SM00407; IGC1; 4 | | |
| DR | SMART; SM00406; IGV; 1 | | |
| DR | SMART; SM00410; IG_ILKE; 1 | | |
| DR | PROSITE; PS00290; IG_MHC; UNKNOWN_3 | | |
| SO | SEQUENCE | 597 AA; | 65300 MW; 2DAFAD50A6375851 CRC64; |
| Query Match | 24.2%; | Score 413; | DB 4; Length 597; |
| Best Local Similarity | 28.7%; | Pred. No. 3.9e-29; | |
| Matches | 94; Conservative | 63; Mismatches | 159; Indels 12; Gaps 8 |

```
QY 3 PPTVKILIOSSCDGGHPPPTIQLCLVSGTTPGINTITWLEDGQVMDVLDSTASTOGE 62
DB 254 PPKVSVFVPPRDGFFGFPKRKSLICQATGFSRQIOVSWLREGQVSGVTTDOVOAEK 313
QY 63 LA-----STOSELTLISQKHWLSDRTYTCOVYOGHTF-EDSTKCCADSNPRGSAVLSRP 116
DB 314 ESGPTTKYKVTSTLIKESDMLISQSMFTCRVDHRLGTFOQANSSMCVDPDQTAIRVFAIRP 373
QY 117 SPEDLFRKSPPTTICLVVDLAPSKGTVNLWTSRASGRPVNHSRKEEKORNGTLTVSTL 176
DB 374 SFASIFLTKSTKLCLVTDLT-TYDSVTISWTRONGEAVKTHNTNISESHPNATFSAVGEA 432
QY 177 PVGRDMIEGEGTCOVRTHPLRALMRSTTKTSGPRA-APEVYAF-ATPEWPSRDKRT 234
DB 433 SICEDDMNSGERFTCTVTHDLPSPILKQTSRPGVALHRRDXYLLPPARQOLNLRSAT 492
QY 235 LACLIQNFMPEDISVQMLHNEVOLPDARHSTTOPR-KTKSGG-FEVFSRLVETRAEWOK 292
DB 493 ITCLVTGFSPADVYVQMMQOGPLSPREKYTSAPMPEQAPGRYFAHSILTVSEEWNTG 552
QY 293 DEFICRAVHEAASPSQTVQRAVSNPGR 320
DB 553 ETYTCVVAHEAL-PNRVTERTVDKSTGK 579
```

RESULT 7

```
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical 65.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-B-CCELL;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1;
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;
```

Query Match 24.2%; Score 413; DB 4; Length 597;

Best Local Similarity 28.7%; Pred. No. 3.9e-29; Matches 94; Conservative 63; Mismatches 159; Indels 12; Gaps 8;

```
QY 3 PPTVKILIOSSCDGGHPPPTIQLCLVSGTTPGINTITWLEDGQVMDVLDSTASTOGE 62
DB 254 PPKVSVFVPPRDGFFGFPKRKSLICQATGFSRQIOVSWLREGQVSGVTTDOVOAEK 313
QY 63 LA-----STOSELTLISQKHWLSDRTYTCOVYOGHTF-EDSTKCCADSNPRGSAVLSRP 116
DB 314 ESGPTTKYKVTSTLIKESDMLISQSMFTCRVDHRLGTFOQANSSMCVDPDQTAIRVFAIRP 373
QY 117 SPEDLFRKSPPTTICLVVDLAPSKGTVNLWTSRASGRPVNHSRKEEKORNGTLTVSTL 176
DB 374 SFASIFLTKSTKLCLVTDLT-TYDSVTISWTRONGEAVKTHNTNISESHPNATFSAVGEA 432
QY 177 PVGRDMIEGEGTCOVRTHPLRALMRSTTKTSGPRA-APEVYAF-ATPEWPSRDKRT 234
DB 433 SICEDDMNSGERFTCTVTHDLPSPILKQTSRPGVALHRRDXYLLPPARQOLNLRSAT 492
QY 235 LACLIQNFMPEDISVQMLHNEVOLPDARHSTTOPR-KTKSGG-FEVFSRLVETRAEWOK 292
DB 493 ITCLVTGFSPADVYVQMMQOGPLSPREKYTSAPMPEQAPGRYFAHSILTVSEEWNTG 552
```

```
QY 293 DEFICRAVHEAASPSQTVQRAVSNPGR 320
DB 553 ETYTCVVAHEAL-PNRVTERTVDKSTGK 579
```

RESULT 8

```
Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Hypothetical 65.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPH;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1;
DR HSSP; P01825; 75AB.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003600; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_5.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGL1; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
```

Query Match 24.2%; Score 413; DB 4; Length 597;
Best Local Similarity 28.7%; Pred. No. 3.9e-29;
Matches 94; Conservative 63; Mismatches 159; Indels 12; Gaps 8;

```
QY 3 PPTVKILIOSSCDGGHPPPTIQLCLVSGTTPGINTITWLEDGQVMDVLDSTASTOGE 62
DB 254 PPKVSVFVPPRDGFFGFPKRKSLICQATGFSRQIOVSWLREGQVSGVTTDOVOAEK 313
QY 63 LA-----STOSELTLISQKHWLSDRTYTCOVYOGHTF-EDSTKCCADSNPRGSAVLSRP 116
DB 314 ESGPTTKYKVTSTLIKESDMLISQSMFTCRVDHRLGTFOQANSSMCVDPDQTAIRVFAIRP 373
QY 117 SPEDLFRKSPPTTICLVVDLAPSKGTVNLWTSRASGRPVNHSRKEEKORNGTLTVSTL 176
DB 374 SFASIFLTKSTKLCLVTDLT-TYDSVTISWTRONGEAVKTHNTNISESHPNATFSAVGEA 432
QY 177 PVGRDMIEGEGTCOVRTHPLRALMRSTTKTSGPRA-APEVYAF-ATPEWPSRDKRT 234
DB 433 SICEDDMNSGERFTCTVTHDLPSPILKQTSRPGVALHRRDXYLLPPARQOLNLRSAT 492
QY 235 LACLIQNFMPEDISVQMLHNEVOLPDARHSTTOPR-KTKSGG-FEVFSRLVETRAEWOK 292
DB 493 ITCLVTGFSPADVYVQMMQOGPLSPREKYTSAPMPEQAPGRYFAHSILTVSEEWNTG 552
QY 293 DEFICRAVHEAASPSQTVQRAVSNPGR 320
DB 553 ETYTCVVAHEAL-PNRVTERTVDKSTGK 579
```

RESULT 9

```
Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
```


DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Gamma heavy chain of Mab7 (Fragment).
 GN IGH-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilde K.G., Yu X., Ekramodoullah A.K.M., Mistra S.;
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
 RT antibody (Mab 7, its light and heavy chains) and construction of a
 RT single chain antibody (scFv)."
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF152372; AAD04243.1; -
 DR HSP: P01842; 7FAB.
 DR MGD: MGI:96446; Igh-4.
 DR InterPro: IPR003600; Ig_like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_4.
 DR SMART: SM00406; IgV_1.
 DR SMART: SM00410; Ig_Like; 2.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 FT NON TER 1 437 1
 FT SEQUENCE 437 AA; 48142 MW; 5C3A7BB3E7D697C CRC64;
 SO
 Query Match 24.1%; Score 411; DB 11; Length 437;
 Best Local Similarity 29.5%; Pred. No. 3.9e-29;
 Matches 97; Conservative 59; Mismatches 155; Indels 18; Gaps 7;
 QY 2 TPPTVTKLQSSCDGGHFPPTIQLCLVSGYPTGINTITWLEDQGVMDVLDSTASTQEG 61
 DB 117 TPSPVYPLAPG--SAAQTNSKVTGLCVKGFPEPVTVW--NSGSLSSGVTTPAVLQS 172
 QY 62 ELASTOSELTLQKHWLSDRTYTCQVYYQGHTE-----EDSTKCADSNRGVSAY 112
 DB 173 DLYTLSSSVTPSTWSE-TVICNVAHNPASTVKDKIYPRDGCACPCICTVEVSSVF 231
 QY 113 LSRSPSPD-LFIRKSPITTCLVNLDAPSKGVNLWTSRASKPVNHSSTREKQRNGTLT 171
 DB 232 IFPPKPRDVLITLTLPKVTGVVDISKDDPEVQSPVDVDEHTAQTQPREEOFNSTFR 291
 QY 172 VTSLPYGTNRDMEGTYGCRVTHPHLPALMRSTTKSGRAPAYAFATPMPGSRD 231
 DB 292 SVSELPIMHODWLNKKEKCRVNSAPAPLEKTIKTKGRKAPQVYITIPPEQMAKD 351
 QY 232 KRTIACLIONFMPEDISVQWLNHEVOLPDARHSTTOPRKTKSGGFVFSRLVTRAEMQ 291
 DB 352 KVSILCMTIDFEPPDIYEWQWN--GQPAENYKNTQPIIMDDSGYFYASKNLVQKSNMEA 409
 QY 292 KDEFCRAVHEAASPSQTVORAVSVNGK 320
 DB 410 GNTFTCSVLHGLHNHHT-EKNLSHSPGK 437
 RESULT 10
 Q8WDX4 PRELIMINARY; PRT; 588 AA.
 AC Q8WDX4;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
 DE 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Hypothetical 64.4 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LYMPH;

RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC019235; AAH19235.1; -
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_5.
 DR SMART: SM00409; Ig_2.
 DR SMART: SM00407; IgC1; 4.
 DR SMART: SM00406; IgV_1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
 KW Hypothetical protein.
 SO SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;
 Query Match 23.7%; Score 404; DB 4; Length 588;
 Best Local Similarity 28.6%; Pred. No. 2.5e-28;
 Matches 92; Conservative 62; Mismatches 156; Indels 12; Gaps 8;
 QY 3 PPVTYKILQSSCDGGHFPPTIQLCLVSGYPTGINTITWLEDQGVMDVLDSTASTQEG 62
 DB 254 PPKVSVVPPRDGFGNPRKSKLICQATGFSPTQIVSWLREKQVSGVTTDOVOAEAK 313
 QY 63 LA-----STOSELTLQKHWLSDRTYTCQVYYQGHTE-----EDSTKCADSNRGVSAYLSRP 116
 DB 314 ESGPTTYKVTSTLIKESDMLQSMFTCRVDHRELFTQQAASSMCVDDQTAIRVFAIP 373
 QY 117 SPFDLFRKSPITTCLVNLDAPSKGVNLWTSRASKPVNHSSTREKQRNGTLTIVSTL 176
 DB 374 SFASIFLTKSTKLCLVTLDTL-TYDSVTISWTRONGAVVTHNTNISHHPATFSAVGEA 432
 QY 177 PVGRDMEGTYGCRVTHPHLPALMRSTTKSGPRA-APEVYAF-ATPEMPGSRDKRT 234
 DB 433 SICEDDMNSGERFTCYTHDLPRLKOTISRPQVALNHRDVLTPRPAQNLRRSAT 492
 QY 493 ITCLVTFGFSPADVQWMMORQPLSPREKYVSAPMPQAPAGRYFAHSILTVSEEWNTG 552
 QY 293 DEFCRAVHEAASPSQTVORAV 314
 DB 553 ETYCVVAHEAL-PNRVTERTV 573
 RESULT 11
 Q96EY0 PRELIMINARY; PRT; 613 AA.
 AC Q96EY0;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DE 01-MAR-2002 (Tremblrel. 20, last annotation update)
 DE Unknown (protein for MGC:20337).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-B-CELL;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC011857; AAH11857.1; -
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_5.
 DR SMART: SM00408; IgC2; 2.
 DR SMART: SM00406; IgV_1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
 KW Immunoglobulin domain.
 SO SEQUENCE 613 AA; 67273 MW; 3121A203FB8421E7 CRC64;
 Query Match 23.7%; Score 404; DB 4; Length 613;
 Best Local Similarity 28.6%; Pred. No. 2.7e-28;
 Matches 92; Conservative 62; Mismatches 156; Indels 12; Gaps 8;

[illegible]

| RESULT 12 | | | |
|-----------|---|--------------|--------------|
| 08MWK1 | | | |
| ID | 08MWK1 | PRELIMINARY; | PRT; 613 AA. |
| DT | 01-MAR-2002 (TREMBLrel, 20, Created) | | |
| DT | 01-MAR-2002 (TREMBLrel, 20, Last sequence update) | | |
| DT | 01-JUN-2002 (TREMBLrel, 21, Last annotation update) | | |
| DE | Hypothetical 67.3 kDa protein. | | |
| OS | Homo sapiens (Human). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. | | |
| OX | NCBI_TaxID=9606; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | TISSUE=TONSIL; | | |
| RA | Strausberg R.; | | |
| RL | Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases. | | |
| DR | EMBL; BC020240; AAH20240.1; - | | |
| DR | InterPro: IPR003599; Ig. | | |
| DR | InterPro: IPR003597; Ig_C1 | | |
| DR | InterPro: IPR003806; Ig_MHC. | | |
| DR | InterPro: IPR003596; Ig_V. | | |
| DR | Pfam: PF00047; Ig_5. | | |
| DR | SMART; SM00409; Ig_2. | | |
| DR | SMART; SM00407; IgC1; 4. | | |
| DR | SMART; SM00406; IGV; 1. | | |
| DR | PROSITE: PS00290; IG_MHC; UNKNOWN_3. | | |
| DR | Hypothetical protein. | | |
| QO | SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64; | | |

| Query Match | Similarity | 23.7% | Score 404 | DB 4 | Length 613 |
|-------------|--------------|---|-------------------|-----------|------------|
| Best Local | Similarity | 28.6% | Pred. No. 2.7e-28 | | |
| Matches | Conservative | 62 | Mismatches 156 | Indels 12 | Gaps 8 |
| QY | 3 | PPTVKILQSSCDGGHFPPTTOLLCLVLGVYPTGNTITWLEDCGVMDVLTASTATGCE | 62 | | |
| Db | 249 | PPKSVYVPPRDGFNGNPKRSKLLCQATGMPFRDIOYSLMEKGVSGYTTDDQYQAEK | 308 | | |
| QY | 63 | LA-----STQSELTLSQKHMLSDRTTYCQVYTGHT-EDSTKRCADSNPBGVAYSIRP | 116 | | |
| Db | 309 | ESGPTTYKAVSTLTIKESDWLSQMFQRCVRDHRLETFQOANSSACVDPDDAIRFAIRP | 368 | | |
| QY | 117 | SPEDLFKRSPTTICLVVDLAPASGNTLMVSRASGPDVYNSTKKEQRQRTLTIVSTL | 176 | | |
| Db | 369 | SFASIFLTKSKTKLCLVTLDTL-TYDSVTISATRONGEAEVKTHTNINISHPNATSAVGEA | 427 | | |
| QY | 177 | PVGTRDMIEGETYQCRVTHPLPRALMRSTTKTSGPRA-APEVAFA-ATPEMPSGRDKRT | 234 | | |

| | | | |
|----------------|-----|--|-----|
| D _b | 428 | SICEDMNSGERTCTVHTDLPSPKQJISPKVALLHRPDVYLLPPARQÜLNRBSAT | 487 |
| Q _y | 235 | LACLIQNEFPEDISVOMLHNEVQLDPARHSTTQPR-KTKSG-FFVSRLEVTAEKÖK | 222 |
| D _b | 488 | ITCLVGFSPADFEVOMORQOPLSPEKYVTSAPMEPOAGRYFAHSILTVSEEWNTG | 547 |
| Q _y | 293 | DEFICRAVHEAASPSOTVORAV | 314 |
| D _b | 548 | EYTCVVAHEAL-PNRVTERIV | 568 |

| | | | |
|--|--------------|------|---------|
| RESULT 13 | | | |
| 096GAB | PRELIMINARY: | PRT: | 614 AA. |
| ID 096GAB | | | |
| AC 096GAB; | | | |
| DT 01-DEC-2001 (TREMBLrel, 19, Created) | | | |
| DT 01-DEC-2001 (TREMBLrel, 19, last sequence update) | | | |
| DT 01-MAR-2002 (TREMBLrel, 20, last annotation update) | | | |
| DE Unknown (protein for MGCL5420). | | | |
| OS Homo sapiens (Human). | | | |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. | | | |
| OX NCBI_TaxID=9606; | | | |
| RN [1] | | | |
| RP SEQUENCE FROM N.A. | | | |
| RS TISSUE=B-CELL; | | | |
| RL Strausberg R.; | | | |
| RA Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases. | | | |
| DR EMBL: BC009851; AAH09851.1; - | | | |
| DR InterPro: IPR000005; HTAARAC. | | | |
| DR InterPro: IPR003598; I9_C2. | | | |
| DR InterPro: IPR003006; I9_MHC. | | | |
| DR Pfam: PF00047; I9; 5... | | | |
| DR SMART: SMO0408; ICG2: 2. | | | |
| DR PROSITE: PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1. | | | |
| DR PROSITE: PS00290; I9_MHC; UNKNOWN_3. | | | |
| DR Immunoglobulin domain. | | | |
| QJ SSOURCE: 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64; | | | |

[illegible]

DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Hypothetical 67.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; AAI17356.1; -
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig_5.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 618 AA; 67758 MW; 96DBDAC7C696E0A6 CRC64;

Query Match 23.7%; Score 404; DB 4; Length 618;
Best Local Similarity 28.6%; Pred. No. 2.7e-28;
Matches 92; Conservative 62; Mismatches 156; Indels 12; Gaps 8;

QY 3 PPVTKIIOSSCDGGHPPTIQLCLVSGYTPGTINTIMLEDOGVMDVLDASTAQGE 62
DB 254 PPKSVTFPPRDGFFGNPRKSKLICQATGFPROIQVMSLREKQVGGVTTDOYQAEAK 313
QY 63 LA----STQSELTLISQKHWLSDRTYTCQVYQGHTE-EDSTKCADSNPRGVASLSRP 116
DB 314 ESGPTTKVVTSTLTIKESDWLSQSMFTCRDHRGTLFQNASMSKVPQDPAIRFEALFP 373
QY 117 SPFLFIKRSPTTICLVVDLAPSKGTVLMTSRASGKRVNHSSTKREKQNGTLVSTL 176
DB 374 SPASIFLTKSTKLCVLDLT-TYDSVTISWTRONGEAVKTHNISESHPATPSAVGEA 432
QY 177 PVGTRDWIEGETYOCRAVTHPHLPALMRSTTKTSGPRA-APEVYAF-ATPPMPSGRDKRT 234
DB 433 SICDDMNKSGERFCTVHTDLPRLKOTISRPKVALHRRDVIYLLPARRQLNIREAT 492
QY 235 LACLIQNFMPEDISVQWLHNEVQLPDARHSTTPR-KTKGSG-PFVFSRLEVTAEWEOK 292
DB 493 ITCLVTFGRSPADVQWQRCQPLSPKXVTSAPMPEDQAPGRYFAHSILTYSEEWNTG 552
QY 293 DEFICRAVHAASPSQVQRAV 314
DB 553 EYTCVVAHEAL-PKRTERTV 573

RESULT 15
099L31
ID 099L31 PRELIMINARY; PRT; 468 AA.
AC 099L31;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Similar to RIKEN cDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAI03878.1; -
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003600; IG_like.
DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 23.6%; Score 402; DB 11; Length 468;
Best Local Similarity 28.6%; Pred. No. 2.8e-28;
Matches 97; Conservative 63; Mismatches 147; Indels 32; Gaps 8;

QY 2 TPPTVKIIOSSCDGGHPPTIQLCLVSGYTPGTINTIMLEDOGVMDVLDASTAQEG 61
DB 142 TAPSVYPLAPVC--GDTTGSVTLGLCLVKGTFPEPVILTW--NSGSLSSGHTTPAVIQS 197
QY 62 ELASTQSELTLISQKHWLSDRTYTCQVYQGHTEFEDSTKCADSNPRGVA----- 111
DB 198 DLYTLSSSVTVSTSTWPS-QSITCNVAHPA-----STKVDKRIEPRGPTIKPCPKCPA 252
QY 112 --YLSRSPF-----DLFIKSPITTCVVDLAPSKGTVNLTMSRASKPVNHSRTRK 161
DB 253 PNLGGPSVFTFPKIKDVLMISSPMVTCVAVVSEDDPDVQISWFVNNVEVLTQOT 312
QY 162 EEKQNGTLVTVSTLPVGTQDMIEGETYOCRAVTHPHLPALMRSTTKTSGPRAPEVYAF 221
DB 313 HREDYNSLRLRVYSALPIQHDMSKKEKCKVNNKALPAPLERTISKKGSVARQYVYL 372
QY 222 ATPMPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTPRKTGSGFVFSR 281
DB 373 PPPEEEMTKKQVTLTCWTDPMPEDIYEVETNN--GKTELNYKNTPEVLDSDGSYFMYSK 430
QY 282 LEVTRAWEOKDEFICRAVHAASPSQVQRAVSNPCK 320
DB 431 LRVKKNVVERNSTSCSVHHEGLNHNHTT-KSFSTPEK 468

Search completed: July 15, 2003, 07:01:48
Job time : 36.9679 secs

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OW protein - protein search, using sw model

Run on: July 15, 2003, 06:59:40 ; Search time 24.5495 Seconds
(without alignments)
1517.518 Million cell updates/sec

Title: US-09-847-208B-6
Perfect score: 1707
Sequence: 1 FTPTVKILQSSCDGCGHFP.....HEAASPSQTVQRAVSVPNGK 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCIT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/PCITUS_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---|
| 1 | 1707 | 100.0 | 320 | 9 | US-09-847-208-6 Sequence 6, Appli |
| 2 | 1707 | 100.0 | 323 | 9 | US-09-949-375A-2 Sequence 2, Appli |
| 3 | 1707 | 100.0 | 323 | 9 | US-09-949-375A-4 Sequence 4, Appli |
| 4 | 1707 | 100.0 | 323 | 9 | US-09-949-375A-6 Sequence 6, Appli |
| 5 | 1707 | 100.0 | 331 | 9 | US-10-176-664-1 Sequence 1, Appli |
| 6 | 1707 | 100.0 | 331 | 9 | US-10-207-655-329 Sequence 329, App |
| 7 | 1707 | 100.0 | 331 | 10 | US-09-401-636-1 Sequence 1, Appli |
| 8 | 1707 | 100.0 | 427 | 9 | US-09-847-208-5 Sequence 5, Appli |
| 9 | 1707 | 100.0 | 428 | 9 | US-10-047-542-60 Sequence 60, Appli |
| 10 | 1707 | 100.0 | 428 | 9 | US-09-949-375A-1 Sequence 1, Appli |
| 11 | 1707 | 100.0 | 428 | 10 | US-09-916-230-1 Sequence 1, Appli |
| 12 | 1707 | 100.0 | 569 | 9 | US-09-847-208-7 Sequence 7, Appli |
| 13 | 1707 | 100.0 | 574 | 9 | US-10-047-542-45 Sequence 45, Appli |
| 14 | 1707 | 100.0 | 574 | 9 | US-10-214-524-37 Sequence 37, Appli |
| 15 | 1707 | 100.0 | 592 | 9 | US-10-207-655-334 Sequence 334, App |
| 16 | 1696 | 99.4 | 532 | 9 | US-09-949-375A-8 Sequence 8, Appli |
| 17 | 1696 | 99.4 | 441 | 9 | US-09-949-375A-7 Sequence 7, Appli |
| 18 | 1671 | 97.9 | 330 | 9 | US-09-949-375A-10 Sequence 10, Appli |
| 19 | 1649 | 96.6 | 347 | 9 | US-10-152-190-13 Sequence 13, Appli |

| | | | | | |
|----|--------|------|-----|----|--|
| 20 | 1644.5 | 96.3 | 426 | 9 | US-10-214-524-26 Sequence 26, Appli |
| 21 | 1579 | 92.5 | 347 | 9 | US-10-152-190-12 Sequence 12, Appli |
| 22 | 1566.5 | 91.8 | 348 | 9 | US-10-152-190-11 Sequence 11, Appli |
| 23 | 1435.5 | 84.1 | 346 | 9 | US-10-152-190-10 Sequence 10, Appli |
| 24 | 1364.5 | 79.9 | 346 | 9 | US-10-152-190-14 Sequence 14, Appli |
| 25 | 1158 | 67.8 | 222 | 9 | US-09-809-715-6 Sequence 6, Appli |
| 26 | 1158 | 67.8 | 222 | 10 | US-09-809-746-2 Sequence 2, Appli |
| 27 | 1038.5 | 60.8 | 342 | 9 | US-10-176-664-8 Sequence 8, Appli |
| 28 | 1038.5 | 60.8 | 342 | 10 | US-09-401-636-8 Sequence 8, Appli |
| 29 | 1011.5 | 59.3 | 236 | 9 | US-10-152-190-9 Sequence 9, Appli |
| 30 | 956.5 | 56.0 | 426 | 9 | US-10-214-524-28 Sequence 28, Appli |
| 31 | 955.5 | 56.0 | 496 | 9 | US-10-214-524-25 Sequence 25, Appli |
| 32 | 949.5 | 55.6 | 431 | 9 | US-09-479-614-14 Sequence 14, Appli |
| 33 | 949.5 | 55.6 | 496 | 9 | US-09-479-614-2 Sequence 2, Appli |
| 34 | 949.5 | 55.6 | 496 | 9 | US-09-479-614-29 Sequence 29, Appli |
| 35 | 906.5 | 53.1 | 569 | 9 | US-10-214-524-30 Sequence 30, Appli |
| 36 | 827 | 48.4 | 341 | 9 | US-10-176-664-11 Sequence 11, Appli |
| 37 | 827 | 48.4 | 341 | 10 | US-09-401-636-11 Sequence 11, Appli |
| 38 | 823 | 48.2 | 563 | 9 | US-10-214-524-35 Sequence 35, Appli |
| 39 | 804 | 47.1 | 567 | 9 | US-10-214-524-33 Sequence 33, Appli |
| 40 | 793 | 46.5 | 340 | 9 | US-10-176-664-2 Sequence 2, Appli |
| 41 | 793 | 46.5 | 340 | 10 | US-09-401-636-2 Sequence 2, Appli |
| 42 | 793 | 46.5 | 428 | 9 | US-10-214-524-34 Sequence 34, Appli |
| 43 | 788.5 | 46.2 | 426 | 9 | US-10-214-524-27 Sequence 27, Appli |
| 44 | 781 | 45.8 | 341 | 9 | US-10-176-664-3 Sequence 3, Appli |
| 45 | 781 | 45.8 | 341 | 10 | US-09-401-636-3 Sequence 3, Appli |

ALIGNMENTS

RESULT 1
US-09-847-208-6
Sequence 6, Application US/09847208
Publication NO. US20030082190A1
GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daocheng
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC61.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens
US-09-847-208-6

| Query Match | Score 1707: | DB 9: | Length 320: |
|-----------------------|--------------|--|---------------|
| Best Local Similarity | 100.0% | Pred. No. 8.3e-122; | |
| Matches 320: | Conservative | 0; | Mismatches 0; |
| | | Indels 0; | Gaps 0; |
| QY | 1 | FTPTVKILQSSCDGCGHFPPTIQLCLVSGTPTGINTTWLEDQVMDVDTASTAQE | 60 |
| DB | 1 | FTPTVKILQSSCDGCGHFPPTIQLCLVSGTPTGINTTWLEDQVMDVDTASTAQE | 60 |
| QY | 61 | GELASTOSELTLSQKHMLSDRTYTCQVYTGHTFEDSTKCADSNPRGVSAVLSRSPPD | 120 |
| DB | 61 | GELASTOSELTLSQKHMLSDRTYTCQVYTGHTFEDSTKCADSNPRGVSAVLSRSPPD | 120 |
| QY | 121 | LFIRKSPITTCVVDLAPSKGVNLTWSASGKPVNHSRKEKORNGTLTSTLPVGT | 180 |
| DB | 121 | LFIRKSPITTCVVDLAPSKGVNLTWSASGKPVNHSRKEKORNGTLTSTLPVGT | 180 |
| QY | 181 | RDWIGETGYOCVTHPHLPALMRSTTKSGRAPEYAFATPMPGSRDKRTACTLQ | 240 |
| DB | 181 | RDWIGETGYOCVTHPHLPALMRSTTKSGRAPEYAFATPMPGSRDKRTACTLQ | 240 |
| QY | 241 | NMPEDISYQWLHNEVQLPDARHSTTQPRKTKSGGFVFSRLEVTTRAWEOKDEFICRAV | 300 |

|||||
Db 241 NFMEDISVOMLHNEVOLPDARHSTTOPRKTKSGFFVFSRLLEVTRAWEQKDEFFICRAV 300
QY 301 HEASPSQTVORAVSNPGK 320
|||||
Db 301 HEASPSQTVORAVSNPGK 320
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RESULT 2
US-09-949-375A-2
; Sequence 2, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-011P
; CURRENT APPLICATION NUMBER: US/09/949, 375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 323
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (8)..(103)
; OTHER INFORMATION: Human IGE heavy chain C2 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (112)..(211)
; OTHER INFORMATION: Human IGE heavy chain C3 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (216)..(317)
; OTHER INFORMATION: Human IGE heavy chain C4 domain
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (104)..(111)
; OTHER INFORMATION: Linker between domains C2 and C3
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (212)..(215)
; OTHER INFORMATION: Linker between domains C3 and C4
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (100)..(114)
; OTHER INFORMATION: Epitope including C2C3 linker
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (210)..(218)
; OTHER INFORMATION: Epitope including C3C4 linker
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (139)..(145)
; OTHER INFORMATION: Epitope in BC loop
; NAME/KEY: MISC_FEATURE
; LOCATION: (167)..(175)
; OTHER INFORMATION: Epitope in DE loop
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (196)..(206)
; OTHER INFORMATION: Epitope in FG loop
; US-09-949-375A-2
Query Match 100.0%; Score 1707; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-122;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDDGVMDVLDLSTASTOE 60
|||||
Db 4 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDDGVMDVLDLSTASTOE 63

QY 61 GELASTOSELTLSQKHWLSDRTYTCQVYTGHTFEDSTKCCADSNPBGVSAYLSRPSFPD 120
|||||
Db 64 GELASTOSELTLSQKHWLSDRTYTCQVYTGHTFEDSTKCCADSNPBGVSAYLSRPSFPD 123
|||||
QY 121 LFIKSPITICLVVDLAPSKGTVNLWTSRSGKRVNHNSTKREKORNGTLLVSTLPVGT 180
|||||
Db 124 LFIKSPITICLVVDLAPSKGTVNLWTSRSGKRVNHNSTKREKORNGTLLVSTLPVGT 183
|||||
QY 181 RDWIEGETYOCRYVHPLPALMRSTTKSGPRAPEVYAFATPEWPGSRDKRTLACLIQ 240
|||||
Db 184 RDWIEGETYOCRYVHPLPALMRSTTKSGPRAPEVYAFATPEWPGSRDKRTLACLIQ 243
|||||
QY 241 NFMEDISVOMLHNEVOLPDARHSTTOPRKTKSGFFVFSRLLEVTRAWEQKDEFFICRAV 300
Db 244 NFMEDISVOMLHNEVOLPDARHSTTOPRKTKSGFFVFSRLLEVTRAWEQKDEFFICRAV 303
|||||
QY 301 HEASPSQTVORAVSNPGK 320
Db 304 HEASPSQTVORAVSNPGK 323
|||||

RESULT 3
US-09-949-375A-4
; Sequence 4, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-011P
; CURRENT APPLICATION NUMBER: US/09/949, 375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 3.
; US-09-949-375A-4
Query Match 100.0%; Score 1707; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-122;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDDGVMDVLDLSTASTOE 60
|||||
Db 4 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDDGVMDVLDLSTASTOE 63
|||||
QY 61 GELASTOSELTLSQKHWLSDRTYTCQVYTGHTFEDSTKCCADSNPBGVSAYLSRPSFPD 120
|||||
Db 64 GELASTOSELTLSQKHWLSDRTYTCQVYTGHTFEDSTKCCADSNPBGVSAYLSRPSFPD 123
|||||
QY 121 LFIKSPITICLVVDLAPSKGTVNLWTSRSGKRVNHNSTKREKORNGTLLVSTLPVGT 180
Db 124 LFIKSPITICLVVDLAPSKGTVNLWTSRSGKRVNHNSTKREKORNGTLLVSTLPVGT 183
|||||
QY 181 RDWIEGETYOCRYVHPLPALMRSTTKSGPRAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 184 RDWIEGETYOCRYVHPLPALMRSTTKSGPRAPEVYAFATPEWPGSRDKRTLACLIQ 243
|||||
QY 241 NFMEDISVOMLHNEVOLPDARHSTTOPRKTKSGFFVFSRLLEVTRAWEQKDEFFICRAV 300
Db 244 NFMEDISVOMLHNEVOLPDARHSTTOPRKTKSGFFVFSRLLEVTRAWEQKDEFFICRAV 303
|||||
QY 301 HEASPSQTVORAVSNPGK 320
Db 304 HEASPSQTVORAVSNPGK 323
|||||

RESULT 4
US-09-949-375A-6

; Sequence 6, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING ICE
; FILE REFERENCE: 3631-0111P
; CURRENT APPLICATION NUMBER: US/09/949,375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 5.
US-09-949-375A-6

Query Match 100.0%; Score 1707; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 8,4e-122;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | FTPTVVKILQSSCGGGHFPPTIQLCLVSGYTGTTITWLEGGQVMDVLDSTASTQ | 60 |
| DB | 4 | FTPTVVKILQSSCGGGHFPPTIQLCLVSGYTGTTITWLEGGQVMDVLDSTASTQ | 63 |
| QY | 61 | GELASTQSELTLSQKHWLSDRTYTCQVYTGHTFEDSTKCKADSNPRGSAVLSRPSFD | 120 |
| DB | 64 | GELASTQSELTLSQKHWLSDRTYTCQVYTGHTFEDSTKCKADSNPRGSAVLSRPSFD | 123 |
| QY | 121 | LFIRKSPITITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLTVSTLPVGT | 180 |
| DB | 124 | LFIRKSPITITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLTVSTLPVGT | 183 |
| QY | 181 | RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYAAATPEMPSSRDKRTIACLIQ | 240 |
| DB | 184 | RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYAAATPEMPSSRDKRTIACLIQ | 243 |
| QY | 241 | NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLLEVTRAEMQKDEFICRAV | 300 |
| DB | 244 | NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLLEVTRAEMQKDEFICRAV | 303 |
| QY | 301 | HEAASPSQTVQRAVSVNPGK | 320 |
| DB | 304 | HEAASPSQTVQRAVSVNPGK | 323 |

RESULT 5
US-10-176-664-1

; Sequence 1, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-1

Query Match 100.0%; Score 1707; DB 9; Length 331;
Best Local Similarity 100.0%; Pred. No. 8,6e-122;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | FTPTVVKILQSSCGGGHFPPTIQLCLVSGYTGTTITWLEGGQVMDVLDSTASTQ | 60 |
| DB | 12 | FTPTVVKILQSSCGGGHFPPTIQLCLVSGYTGTTITWLEGGQVMDVLDSTASTQ | 71 |
| QY | 61 | GELASTQSELTLSQKHWLSDRTYTCQVYTGHTFEDSTKCKADSNPRGSAVLSRPSFD | 120 |
| DB | 72 | GELASTQSELTLSQKHWLSDRTYTCQVYTGHTFEDSTKCKADSNPRGSAVLSRPSFD | 131 |
| QY | 121 | LFIRKSPITITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLTVSTLPVGT | 180 |
| DB | 132 | LFIRKSPITITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLTVSTLPVGT | 191 |
| QY | 181 | RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYAAATPEMPSSRDKRTIACLIQ | 240 |
| DB | 192 | RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYAAATPEMPSSRDKRTIACLIQ | 251 |
| QY | 241 | NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLLEVTRAEMQKDEFICRAV | 300 |
| DB | 252 | NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLLEVTRAEMQKDEFICRAV | 311 |
| QY | 301 | HEAASPSQTVQRAVSVNPGK | 320 |
| DB | 312 | HEAASPSQTVQRAVSVNPGK | 331 |

RESULT 6
US-10-207-655-329

; Sequence 329, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Hayden-Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 329
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-329

Query Match 100.0%; Score 1707; DB 9; Length 331;
Best Local Similarity 100.0%; Pred. No. 8,6e-122;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | FTPTVVKILQSSCGGGHFPPTIQLCLVSGYTGTTITWLEGGQVMDVLDSTASTQ | 60 |
| DB | 8 | FTPTVVKILQSSCGGGHFPPTIQLCLVSGYTGTTITWLEGGQVMDVLDSTASTQ | 67 |
| QY | 61 | GELASTQSELTLSQKHWLSDRTYTCQVYTGHTFEDSTKCKADSNPRGSAVLSRPSFD | 120 |
| DB | 68 | GELASTQSELTLSQKHWLSDRTYTCQVYTGHTFEDSTKCKADSNPRGSAVLSRPSFD | 127 |
| QY | 121 | LFIRKSPITITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLTVSTLPVGT | 180 |
| DB | 128 | LFIRKSPITITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLTVSTLPVGT | 187 |
| QY | 181 | RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYAAATPEMPSSRDKRTIACLIQ | 240 |
| DB | 188 | RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYAAATPEMPSSRDKRTIACLIQ | 247 |
| QY | 241 | NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLLEVTRAEMQKDEFICRAV | 300 |
| DB | 248 | NFMEDISVQMLHNEVOLPDARHSTTOPRKTGSGFEVFSRLLEVTRAEMQKDEFICRAV | 307 |
| QY | 301 | HEAASPSQTVQRAVSVNPGK | 320 |

|||||
Db 308 HEAASPSQTVQRAVSVPNGK 327

RESULT 7

US-09-401-636-1
Sequence 1, Application US/09401636

Patent No. US20010038843A1

GENERAL INFORMATION:

APPLICANT: Hellman, Lars T.

TITLE OF INVENTION: ENHANCED VACCINES

FILE REFERENCE: 10223/006001

CURRENT APPLICATION NUMBER: US/09/401.636

PRIOR FILING DATE: 1999-09-22

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 331

TYPE: PR

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetically generated proteins

US-09-401-636-1

Query Match

Best Local Similarity 100.0%; Score 1707; DB 10; Length 331;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FTPTVKIIQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDSTASTOE 60

12 FTPTVKIIQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDSTASTOE 71

61 GELASTOSELTLQSKHMLSDRTYTCQYTGHTFEDSTKCAASNPRGVSAYLSRSPFD 120

72 GELASTOSELTLQSKHMLSDRTYTCQYTGHTFEDSTKCAASNPRGVSAYLSRSPFD 131

121 LFTKSPITICLVVDLAPSKGYNLWTSRASGKPVNSTKREKORNGTLTVSTLPVGT 180

132 LFTKSPITICLVVDLAPSKGYNLWTSRASGKPVNSTKREKORNGTLTVSTLPVGT 191

181 RDWIEGTTCRVTHPHLPALMRSTTKTGSPRAAPEVYAFAPPEWGSBDKRTLACLIQ 240

192 RDWIEGTTCRVTHPHLPALMRSTTKTGSPRAAPEVYAFAPPEWGSBDKRTLACLIQ 251

241 NFMPEDISVQMLHNEVQLPDARHSTQPRKTKSGFVFESRLLEVTRAEMQKDEFTICRAV 300

252 NFMPEDISVQMLHNEVQLPDARHSTQPRKTKSGFVFESRLLEVTRAEMQKDEFTICRAV 311

301 HEAASPSQTVQRAVSVPNGK 320

312 HEAASPSQTVQRAVSVPNGK 331

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

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QY

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Db

QY

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QY

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QY

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QY

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QY

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QY

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QY

Db

QY

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QY

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QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

ORGANISM: Homo sapiens
US-09-847-208-5

Query Match
Best Local Similarity 100.0%; Score 1707; DB 9; Length 427;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FTPTVKIIQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDSTASTOE 60

108 FTPTVKIIQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDSTASTOE 167

61 GELASTOSELTLQSKHMLSDRTYTCQYTGHTFEDSTKCAASNPRGVSAYLSRSPFD 120

168 GELASTOSELTLQSKHMLSDRTYTCQYTGHTFEDSTKCAASNPRGVSAYLSRSPFD 227

121 LFTKSPITICLVVDLAPSKGYNLWTSRASGKPVNSTKREKORNGTLTVSTLPVGT 180

228 LFTKSPITICLVVDLAPSKGYNLWTSRASGKPVNSTKREKORNGTLTVSTLPVGT 287

181 RDWIEGTTCRVTHPHLPALMRSTTKTGSPRAAPEVYAFAPPEWGSBDKRTLACLIQ 240

288 RDWIEGTTCRVTHPHLPALMRSTTKTGSPRAAPEVYAFAPPEWGSBDKRTLACLIQ 347

241 NFMPEDISVQMLHNEVQLPDARHSTQPRKTKSGFVFESRLLEVTRAEMQKDEFTICRAV 300

348 NFMPEDISVQMLHNEVQLPDARHSTQPRKTKSGFVFESRLLEVTRAEMQKDEFTICRAV 407

301 HEAASPSQTVQRAVSVPNGK 320

408 HEAASPSQTVQRAVSVPNGK 427

Db

QY

Db

QY

Db

QY

Db

QY

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QY

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QY

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QY

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QY

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QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

|||||
Db 289 RDWIEGETYQCRVTHPHLPALMRSTTKSGPRAPEVYATPEWPGSRDKRTLACLIQ 348
QY 241 NFMEDISVQWLHNEVOLPDARHSTTOPRKTKSGFFVFSLEVTYRAEMEKDEFICRAV 300
Db 349 NFMEDISVQWLHNEVOLPDARHSTTOPRKTKSGFFVFSLEVTYRAEMEKDEFICRAV 408
QY 301 HEAASPSQTVORAVSVNPGK 320
Db 409 HEAASPSQTVORAVSVNPGK 428
|||||
RESULT 10
US-09-949-375A-1
; Sequence 1, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-0111P
; CURRENT APPLICATION NUMBER: US/09/949,375A
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 428
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (11)..(116)
; OTHER INFORMATION: Human Ige heavy chain C1 domain
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (209)..(216)
; OTHER INFORMATION: Linker between domains C2 and C3
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (205)..(219)
; OTHER INFORMATION: Epitope including C2C3 linker
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (244)..(251)
; OTHER INFORMATION: Epitope in BC loop
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (272)..(280)
; OTHER INFORMATION: Epitope in DE loop
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (301)..(311)
; OTHER INFORMATION: Epitope in FG loop
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (317)..(320)
; OTHER INFORMATION: Linker between domains C3 and C4
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (321)..(422)
; OTHER INFORMATION: Human Ige heavy chain C4 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (217)..(316)
; OTHER INFORMATION: Human Ige heavy chain C3 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (113)..(208)
; OTHER INFORMATION: Human Ige heavy chain C2 domain
US-09-949-375A-1

Query Match 100.0%; Score 1707; DB 9; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.2e-121;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTPTPVKILQSSCDGGGHFPPTIQLCLVSGTPTGNTITWLEGGQVMDVDLSTASTQOE 60
Db 109 FTPTPVKILQSSCDGGGHFPPTIQLCLVSGTPTGNTITWLEGGQVMDVDLSTASTQOE 168
QY 61 GELASTQSELTLQSKHMLSDRTYTCQVYTGCHTFEDSTKCADSNPRGVSAYLSRPSFD 120
Db 169 GELASTQSELTLQSKHMLSDRTYTCQVYTGCHTFEDSTKCADSNPRGVSAYLSRPSFD 228
QY 121 LFIKRSPTITCLVVDLAPSKGTVNLTWMSRAGKPVNHSRKEEKORNGTLVTSTLPVGT 180
Db 229 LFIKRSPTITCLVVDLAPSKGTVNLTWMSRAGKPVNHSRKEEKORNGTLVTSTLPVGT 288
QY 181 RDWIEGETYQCRVTHPHLPALMRSTTKSGPRAPEVYATPEWPGSRDKRTLACLIQ 240
Db 289 RDWIEGETYQCRVTHPHLPALMRSTTKSGPRAPEVYATPEWPGSRDKRTLACLIQ 348
QY 241 NFMEDISVQWLHNEVOLPDARHSTTOPRKTKSGFFVFSLEVTYRAEMEKDEFICRAV 300
Db 349 NFMEDISVQWLHNEVOLPDARHSTTOPRKTKSGFFVFSLEVTYRAEMEKDEFICRAV 408
QY 301 HEAASPSQTVORAVSVNPGK 320
Db 409 HEAASPSQTVORAVSVNPGK 428
|||||

RESULT 11
US-09-916-230-1
; Sequence 1, Application US/09916230
; Patent No. US20020146422A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Compositions for Inducing Self-Specific Anti-Ige
; FILE REFERENCE: 1700.0140001
; CURRENT APPLICATION NUMBER: US/09/916,230
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/221,841
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-916-230-1

Query Match 100.0%; Score 1707; DB 10; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.2e-121;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTPTPVKILQSSCDGGGHFPPTIQLCLVSGTPTGNTITWLEGGQVMDVDLSTASTQOE 60
Db 109 FTPTPVKILQSSCDGGGHFPPTIQLCLVSGTPTGNTITWLEGGQVMDVDLSTASTQOE 168
QY 61 GELASTQSELTLQSKHMLSDRTYTCQVYTGCHTFEDSTKCADSNPRGVSAYLSRPSFD 120
Db 169 GELASTQSELTLQSKHMLSDRTYTCQVYTGCHTFEDSTKCADSNPRGVSAYLSRPSFD 228
QY 121 LFIKRSPTITCLVVDLAPSKGTVNLTWMSRAGKPVNHSRKEEKORNGTLVTSTLPVGT 180
Db 229 LFIKRSPTITCLVVDLAPSKGTVNLTWMSRAGKPVNHSRKEEKORNGTLVTSTLPVGT 288
QY 181 RDWIEGETYQCRVTHPHLPALMRSTTKSGPRAPEVYATPEWPGSRDKRTLACLIQ 240
Db 289 RDWIEGETYQCRVTHPHLPALMRSTTKSGPRAPEVYATPEWPGSRDKRTLACLIQ 348
QY 241 NFMEDISVQWLHNEVOLPDARHSTTOPRKTKSGFFVFSLEVTYRAEMEKDEFICRAV 300

|||||
Db 349 NFMEDISVOMLHNEVOLDPARHSTTOPRKTKSGGFVFSRLLEVTRAEMQKDEFICRAV 408
QY 301 HEASPSQTVORAVSNPGR 320
|||||
Db 409 HEASPSQTVORAVSNPGR 428

RESULT 12

US-09-847-208-7
; Sequence 7, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67 002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4
; OTHER INFORMATION: (Ige)
US-09-847-208-7

Query Match 100.0%; Score 1707; DB 9; Length 569;
Best Local Similarity 100.0%; Pred. No. 1.6e-121;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKIILSSCDGGHFPPTIQLCLVSGYPTGNTINIMLEDDGVMDVLDLASTTQ 60
|||||
Db 250 FTPTVKIILSSCDGGHFPPTIQLCLVSGYPTGNTINIMLEDDGVMDVLDLASTTQ 309
61 GELASTQSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCADSNPRGSAVLSRPSFD 120
|||||
Db 310 GELASTQSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCADSNPRGSAVLSRPSFD 369
121 LFIKRSPTITCLVVDLAPSKGYVNLWTSRASKPVNHSKKEKORNGITLVSTLPVGT 180
|||||
Db 370 LFIKRSPTITCLVVDLAPSKGYVNLWTSRASKPVNHSKKEKORNGITLVSTLPVGT 429
181 RDMIEGTYOCRTYHPLPRALMSTKTSGRAPAEVYAFATPEWGSRDKRTLACLIQ 240
|||||
Db 430 RDMIEGTYOCRTYHPLPRALMSTKTSGRAPAEVYAFATPEWGSRDKRTLACLIQ 489
241 NFMEDISVOMLHNEVOLDPARHSTTOPRKTKSGGFVFSRLLEVTRAEMQKDEFICRAV 300
|||||
Db 490 NFMEDISVOMLHNEVOLDPARHSTTOPRKTKSGGFVFSRLLEVTRAEMQKDEFICRAV 549
QY 301 HEASPSQTVORAVSNPGR 320
|||||
Db 550 HEASPSQTVORAVSNPGR 569

RESULT 13

US-10-047-542-45
; Sequence 45, Application US/10047542
; Patent No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26

; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-45

Query Match 100.0%; Score 1707; DB 9; Length 574;
Best Local Similarity 100.0%; Pred. No. 1.6e-121;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKIILSSCDGGHFPPTIQLCLVSGYPTGNTINIMLEDDGVMDVLDLASTTQ 60
|||||
Db 255 FTPTVKIILSSCDGGHFPPTIQLCLVSGYPTGNTINIMLEDDGVMDVLDLASTTQ 314
61 GELASTQSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCADSNPRGSAVLSRPSFD 120
|||||
Db 315 GELASTQSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCADSNPRGSAVLSRPSFD 374
121 LFIKRSPTITCLVVDLAPSKGYVNLWTSRASKPVNHSKKEKORNGITLVSTLPVGT 180
|||||
Db 375 LFIKRSPTITCLVVDLAPSKGYVNLWTSRASKPVNHSKKEKORNGITLVSTLPVGT 434
181 RDMIEGTYOCRTYHPLPRALMSTKTSGRAPAEVYAFATPEWGSRDKRTLACLIQ 240
|||||
Db 435 RDMIEGTYOCRTYHPLPRALMSTKTSGRAPAEVYAFATPEWGSRDKRTLACLIQ 494
241 NFMEDISVOMLHNEVOLDPARHSTTOPRKTKSGGFVFSRLLEVTRAEMQKDEFICRAV 300
|||||
Db 495 NFMEDISVOMLHNEVOLDPARHSTTOPRKTKSGGFVFSRLLEVTRAEMQKDEFICRAV 554
QY 301 HEASPSQTVORAVSNPGR 320
|||||
Db 555 HEASPSQTVORAVSNPGR 574

RESULT 14

US-10-214-524-37
; Sequence 37, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swey-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 37
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Human (Homo sapiens)
US-10-214-524-37

Query Match 100.0%; Score 1707; DB 9; Length 574;
Best Local Similarity 100.0%; Pred. No. 1.6e-121;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKIILSSCDGGHFPPTIQLCLVSGYPTGNTINIMLEDDGVMDVLDLASTTQ 60
|||||
Db 255 FTPTVKIILSSCDGGHFPPTIQLCLVSGYPTGNTINIMLEDDGVMDVLDLASTTQ 314
61 GELASTQSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCADSNPRGSAVLSRPSFD 120

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Db      315  GELASTQSELTLSQKHWLSDRTYCCQYTGHTFEDSTKKCADSNPRGVSAYLSRPSFPD 374
QY      121  LFIKRSPTITCLVVDLAPSKGTVNLWTSRASGKPVNHSRKEKQRNGTLVTSTLPVGT 180
Db      375  LFIKRSPTITCLVVDLAPSKGTVNLWTSRASGKPVNHSRKEKQRNGTLVTSTLPVGT 434
QY      181  RDWIEGTYOCRTVHPHLPRALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db      435  RDWIEGTYOCRTVHPHLPRALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 494
QY      241  NFMEDISVQWLHNEVOLPDARHSTTOPRKTGSGFFVFSRLEVTYRAWEQKDEFICRAV 300
Db      495  NFMEDISVQWLHNEVOLPDARHSTTOPRKTGSGFFVFSRLEVTYRAWEQKDEFICRAV 554
QY      301  HEAASPSQTVQRAVSVNPGK 320
Db      555  HEAASPSQTVQRAVSVNPGK 574
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RESULT 15

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US-10-207-655-334
; Sequence 334, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Leadbetter, Jeffrey A.
; APPLICANT: Hayden-Leadbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 334
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-334
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Query Match 100.0%; Score 1707; DB 9; Length 592;

Best Local Similarity 100.0%; Pred. No. 1.7e-121;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1  FTPTVTKILQSSCCGGGHFPTTQLCLVSGYTGCTINITWLEDQVMDVDLSTASTTQE 60
Db      273  FTPTVTKILQSSCCGGGHFPTTQLCLVSGYTGCTINITWLEDQVMDVDLSTASTTQE 332
QY      61  GELASTQSELTLSQKHWLSDRTYCCQYTGHTFEDSTKKCADSNPRGVSAYLSRPSFPD 120
Db      333  GELASTQSELTLSQKHWLSDRTYCCQYTGHTFEDSTKKCADSNPRGVSAYLSRPSFPD 392
QY      121  LFIKRSPTITCLVVDLAPSKGTVNLWTSRASGKPVNHSRKEKQRNGTLVTSTLPVGT 180
Db      393  LFIKRSPTITCLVVDLAPSKGTVNLWTSRASGKPVNHSRKEKQRNGTLVTSTLPVGT 452
QY      181  RDWIEGTYOCRTVHPHLPRALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db      453  RDWIEGTYOCRTVHPHLPRALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 512
QY      241  NFMEDISVQWLHNEVOLPDARHSTTOPRKTGSGFFVFSRLEVTYRAWEQKDEFICRAV 300
Db      513  NFMEDISVQWLHNEVOLPDARHSTTOPRKTGSGFFVFSRLEVTYRAWEQKDEFICRAV 572
QY      301  HEAASPSQTVQRAVSVNPGK 320
Db      573  HEAASPSQTVQRAVSVNPGK 592
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Search completed: July 15, 2003, 07:17:19
Job time : 25.5495 secs

Db 164 EGNATSTHSELINTIÖGEWVSQKTYTTCOYTÖGFTFKDARKCSDDPGVTSTYLSPPSL 223
Qy 120 DLFRKSPPTITCLVVDLAPSKGTYNLAWSRASGKPVNHSRKEKORNGTLTVTSTLPVG 179
Db 224 DLYHAKAPKITCLVVDLDTMKG-NLWTMYRESKKEPVNGLPKNDHFNGITTVTSTLPVN 282
Qy 180 TRDMEGETTCCRYTHPHLPALMRSTTKISGPRAPEVYAFAP-EMPGSRDKRTIACL 238
Db 283 TNDMEGETTCCRYTHPHLPALMRSTTKISGPRAPEVYAFAP-EMPGSRDKRTIACL 342
Qy 239 IONFMPEDISVQWLHNEVQLDARHSTTOPRKTGS--GFVFSRLVETRAEMWOKDEFI 296
Db 343 IONFMPEDISVQWLHNEVQLDARHSTTOPRKTGS--GFVFSRLVETRAEMWOKDEFI 402
Qy 297 CRAVHEAASPSQTVORAVSNPGR 320
Db 403 CQVYHEALSGSRILQKMWSKTPGR 426

RESULT 2

PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYOR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-13795-2

Query Match 56.0%; Score 956.5; DB 5; Length 426;
Best Local Similarity 56.2%; Pred. No. 4.5e-84;
Matches 182; Conservative 50; Mismatches 87; Indels 5; Gaps 4;

Qy 1 FTPTVRLIÖSSCDGGHFPPTIÖLLCLVSGYTPGTINITWLDEQ--VMDVLTASTATQ 59
Db 104 FIPTVRLIÖSSCDGGHFPPTIÖLLCLVSGYTPGTINITWLDEQ--VMDVLTASTATQ 163
Qy 60 EGEIATÖSELTLSÖKHWLSDRTYTCOVYTGHTFEDSTKCKADSNPRGSAVLSRPSPF 119
Db 164 EGNATSTHSELINTIÖGEWVSQKTYTTCOYTÖGFTFKDARKCSDDPGVTSTYLSPPSL 223
Qy 120 DLFRKSPPTITCLVVDLAPSKGTYNLAWSRASGKPVNHSRKEKORNGTLTVTSTLPVG 179

Db 224 DLYHAKAPKITCLVVDLDTMKG-NLWTMYRESKKEPVNGLPKNDHFNGITTVTSTLPVN 282
Qy 180 TRDMEGETTCCRYTHPHLPALMRSTTKISGPRAPEVYAFAP-EMPGSRDKRTIACL 238
Db 283 TNDMEGETTCCRYTHPHLPALMRSTTKISGPRAPEVYAFAP-EMPGSRDKRTIACL 342
Qy 239 IONFMPEDISVQWLHNEVQLDARHSTTOPRKTGS--GFVFSRLVETRAEMWOKDEFI 296
Db 343 IONFMPEDISVQWLHNEVQLDARHSTTOPRKTGS--GFVFSRLVETRAEMWOKDEFI 402
Qy 297 CRAVHEAASPSQTVORAVSNPGR 320
Db 403 CQVYHEALSGSRILQKMWSKTPGR 426

RESULT 3

US-09-192-545-2
; Sequence 2, Application US/09192545
; Patent No. 6118044
; GENERAL INFORMATION:
; APPLICANT: Karasuyama, Hajime
; APPLICANT: Yonekawa, Hiromichi
; APPLICANT: Taya, Choji
; APPLICANT: Matsuo, Kunie
; TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
; FILE REFERENCE: 799P79570
; CURRENT APPLICATION NUMBER: US/09/192,545
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: JP HEI 9-313969
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Designed heavy
US-09-192-545-2

Query Match 39.7%; Score 678.5; DB 3; Length 561;
Best Local Similarity 43.7%; Pred. No. 4.4e-57;
Matches 136; Conservative 56; Mismatches 112; Indels 7; Gaps 6;

Qy 13 CDGGHFPPTIÖLLCLVSGYTPGTINITWL-EDQVMDVLTASTATQEGELASÖSELT 71
Db 247 CDPNA-FHSTIÖLCFYIGHILNDVSVSMILDDREITDTLAÖTILKEEGKLASTCSKLN 305
Qy 72 LÖKHNLSDRTYTCOVYTGHTFEDSTKCKADSNPRGSAVLSRPSPFIRKSPITTC 131
Db 306 ITÖÖMMSESTFTCRVTSÖQGVYLAHTRCPDHEPRGATITLIPSPDLÖKÖNGAPKLTG 365
Qy 132 LVVDLAPSKGTYNLAWSRASGKPVNHSRKEKORNGTLTVTSTLPVTRDMEGETYÖC 191
Db 366 LVVDLESK-NVNTTWÖDEKTSVSASÖWYTKHNNATSTITSLIPYAKMIGYÖC 424
Qy 192 RYTHPHLPALMRSTTKIS--GPRAPEVYAFATPEWPGSRDKRTIACLIONFMPEDISVQ 250
Db 425 VVDRPDPFKPIYRSITLIPÖVSÖRSAPAEYVPPPE-ESEDEKRTIÖLIONFMPEDISVQ 483
Qy 251 WLHNEVQLDARHSTTOPRKTGS--GFVFSRLVETRAEMWOKDEFCRAVHEAASPSQ 308
Db 484 WLÖGÖKLSLNSÖHSTTPPLASNGSÖGFFIRLEVAKTÖKÖFTCOVYHEALÖKPR 543
Qy 309 TVÖRAVSNPGR 319
Db 544 KLEKTIÖTSLG 554

RESULT 4

US-08-232-539D-56
; Sequence 56, Application US/08232539D
; Patent No. 5965709

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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,106A
FILING DATE: 01-Mar-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: P0927
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-399-106A-6

Query Match 34.4%; Score 587; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 2,7e-49;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GPRAPVYVFAFPEWGSRRKRLACLQFMFEDISYQWLHNEVQLPDARHSTGP RK 270
Db 1 GPRAPVYVFAFPEWGSRRKRLACLQFMFEDISYQWLHNEVQLPDARHSTGP RK 60

QY 271 TKGSGFEVFSRLLEVTRAEMEQKDEFICRAVHEAASPSQTVORAVSVNPK 320
Db 61 TKGSGFEVFSRLLEVTRAEMEQKDEFICRAVHEAASPSQTVORAVSVNPK 110

RESULT 6
US-08-433-105A-6
; Sequence 6, Application US/08433105A
; Patent No. 5807706
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Ridgway, John B.
; TITLE OF INVENTION: A METHOD FOR MAKING HETEROMULTIMERIC POLYPEPTIDES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,105A
FILING DATE: 03-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/399106
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: P0927DZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168

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;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 110 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-08-433-105A-6

Query Match 34.4%; Score 587; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 2.7e-49;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GPPAAPVYAFATPEWGSRDKRTLACLIONFMPEDISVOMLHNEVOLPDARHSTQPRK 270
DB 1 GPPAAPVYAFATPEWGSRDKRTLACLIONFMPEDISVOMLHNEVOLPDARHSTQPRK 60

QY 271 TKSGFEVFSRLLEYTRAWEQKDEFICRAVHEAASPSQTVQRAVSNVPGK 320
DB 61 TKSGFEVFSRLLEYTRAWEQKDEFICRAVHEAASPSQTVQRAVSNVPGK 110

RESULT 7

US-08-434-869A-6
; Sequence 6, Application US/08434869A
; Patent No. 5821333

;; GENERAL INFORMATION:
;; APPLICANT: Carter, Paul J.
;; APPLICANT: Presta, Leonard G.
;; APPLICANT: Riddway, John B.
;; TITLE OF INVENTION: A METHOD FOR MAKING HETEROMULTIMERIC POLYPEPTIDES
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Genentech, Inc.
;; STREET: 460 Point San Bruno Blvd
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Mapatin (Genentech)
;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/434,869A
;; FILING DATE: 03-May-1995
;; CLASSIFICATION: 424

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/399106
;; FILING DATE: 01-MAR-1995

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER: 00,000

;; REFERENCE/DOCKET NUMBER: P0927D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/225-1994

;; TELEFAX: 415/952-9881
;; TELEEX: 910/371-7168

;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 110 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear

US-08-434-869A-6

Query Match 34.4%; Score 587; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 2.7e-49;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GPPAAPVYAFATPEWGSRDKRTLACLIONFMPEDISVOMLHNEVOLPDARHSTQPRK 270
DB 1 GPPAAPVYAFATPEWGSRDKRTLACLIONFMPEDISVOMLHNEVOLPDARHSTQPRK 60

QY 271 TKSGFEVFSRLLEYTRAWEQKDEFICRAVHEAASPSQTVQRAVSNVPGK 320

DB 61 TKSGFEVFSRLLEYTRAWEQKDEFICRAVHEAASPSQTVQRAVSNVPGK 110

RESULT 8
US-08-037-579A-2

;; Sequence 2, Application US/08037579A
;; Patent No. 5552537
;; GENERAL INFORMATION:
;; APPLICANT: Zhang, Ke
;; APPLICANT: Max, Edward E
;; APPLICANT: Saxon, Andrew
;; TITLE OF INVENTION: IGE ISOFORMS AND METHODS OF USE
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
;; STREET: 4 Embarcadero Center, Suite 3400
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-4187

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/037,579A
;; FILING DATE: 24-MAR-1993
;; CLASSIFICATION: 424

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rowland, Berttram I
;; REGISTRATION NUMBER: 20,015

;; REFERENCE/DOCKET NUMBER: A-57950/BIR UCLA-233
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 781-1989

;; TELEFAX: (415) 398-3249
;; TELEEX: 910 277299 FHT UR

;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 109 amino acids
;; TYPE: amino acid
;; TOPOLOGY: Linear

;; MOLECULE TYPE: protein
US-08-037-579A-2

Query Match 34.0%; Score 581; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 1e-48;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 PRAAPVYAFATPEWGSRDKRTLACLIONFMPEDISVOMLHNEVOLPDARHSTQPRK 271
DB 1 PRAAPVYAFATPEWGSRDKRTLACLIONFMPEDISVOMLHNEVOLPDARHSTQPRK 60

QY 272 KSGFEVFSRLLEYTRAWEQKDEFICRAVHEAASPSQTVQRAVSNVPGK 320
DB 61 KSGFEVFSRLLEYTRAWEQKDEFICRAVHEAASPSQTVQRAVSNVPGK 109

RESULT 9
US-08-601-184-2

;; Sequence 2, Application US/08601184
;; Patent No. 6043345
;; GENERAL INFORMATION:
;; APPLICANT: Zhang, Ke

;; APPLICANT: Max, Edward E
;; APPLICANT: Saxon, Andrew
;; TITLE OF INVENTION: IGE ISOFORMS AND METHODS OF USE
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
;; STREET: 4 Embarcadero Center, Suite 3400
;; CITY: San Francisco


```
STATE: California
COUNTRY: USA
ZIP: 94114187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,184
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A-57950-1/PJS UCLA233-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-601-184-2

Query Match          34.0%; Score 581; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 1e-48;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 212 PRAAEVAFATPEPGSRDKRTLACLIQNFMPEDISVQWLNENEQLDPARSTTQPKRT 271
DB 1 PRAAEVAFATPEPGSRDKRTLACLIQNFMPEDISVQWLNENEQLDPARSTTQPKRT 60
OY 272 KSGGFVFSRLVETRAEWEQKDEFTICRAVHEAASPSQTVQRAVSNPGK 320
DB 61 KSGGFVFSRLVETRAEWEQKDEFTICRAVHEAASPSQTVQRAVSNPGK 109

RESULT 10
US-08-466-163B-1
; Sequence 1, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-466-163B-1

Query Match          33.2%; Score 566.5; DB 4; Length 109;
Best Local Similarity 99.1%; Pred. No. 2.5e-47;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 103 DSNPGVSAVLSRPSFDLFIKRSPTITCLVVDLAPSKGTWLTMSRASGKPVNHSTKRE 162
|||||
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DB 1 DSNPGVSAVLSRPSFDLFIKRSPTITCLVVDLAPSKGTWLTMSRASGKPVNHSTKRE 60
OY 163 EKORNGTLVTSTLPVGTBMDIEGETYOCVTHPHLPALMRSTTKTSGP 212
DB 61 EKORNGTLVTSTLPVGTBMDIEGETYOCVTHPHLPALMRSTTKTSGP 109

RESULT 11
US-08-232-539D-54
; Sequence 54, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: IGF Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Syoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/352-9881
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: Amino Acid
; TOPOLOGY: linear
US-08-232-539D-54

Query Match          32.6%; Score 556; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5e-46;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 108 GVSATLSRPSFDLFIKRSPTITCLVVDLAPSKGTWLTMSRASGKPVNHSTKREKOR 167
DB 1 GVSATLSRPSFDLFIKRSPTITCLVVDLAPSKGTWLTMSRASGKPVNHSTKREKOR 60
OY 168 GTLVVSTLPLVGTBMDIEGETYOCVTHPHLPALMRSTTKTSGP 212
DB 61 GTLVVSTLPLVGTBMDIEGETYOCVTHPHLPALMRSTTKTSGP 105

RESULT 12
US-08-464-025A-1
; Sequence 1, Application US/08464025A
; Patent No. 5994514
; GENERAL INFORMATION:
; APPLICANT: Jardieu et al.
; TITLE OF INVENTION: IMMUNOGLOBULIN VARIANTS
; NUMBER OF SEQUENCES: 27
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/464,025A
;; FILING DATE: 05-Jun-1995
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Svoboda, Craig G.
;; REGISTRATION NUMBER: 39,044
;; REFERENCE/DOCKET NUMBER: P0718C3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/952-9881
;; TELEFAX: 650/225-1489
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;;
US-08-464-025A-1
;;
Query Match 30.8%; Score 526; DB 2; Length 119;
Best Local Similarity 90.7%; Pred. No. 2.3e-43;
Matches 107; Conservative 1; Mismatches 2; Indels 8; Gaps 4;
;;
QY 103 DSNPRGVSAVLSRSPDP-LFIRKSPITTCLVVDLAPSKGTVNLWTSRAS---GKPVNHS 158
DB 2 DSNPRGVSAVLSRSPDXLFIRKSPITTCLVVDLAPSKGTVNLWTSRXXSXKGPVNH 61
DB 62 TRREKQRXNXXGTLVTVSTLPVGTWIEGTYQCRVTHPLRALXMRSTYTSGP 119
;;
RESULT 13
US-08-466-151-1
;; Sequence 1, Application US/08466151
;; Patent No. 6037453
;; GENERAL INFORMATION:
;; APPLICANT: Jarreau, Paula M.
;; APPLICANT: Presta, Leonard G.
;; TITLE OF INVENTION: Immunoglobulin Variants
;; NUMBER OF SEQUENCES: 65
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/466,151
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/466163
;; FILING DATE: 06-Jun-1995
;; APPLICATION NUMBER: 08/405617
;; FILING DATE: 15-MAR-1995

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/185899
;; FILING DATE: 26-JAN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/879495
;; FILING DATE: 07-MAY-1992
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/744768
;; FILING DATE: 14-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Svoboda, Craig G.
;; REGISTRATION NUMBER: 39,044
;; REFERENCE/DOCKET NUMBER: P0718P2C1D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/952-9881
;; TELEFAX: 650/225-1489
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 118 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;;
US-08-466-151-1
;;
Query Match 29.8%; Score 508.5; DB 3; Length 118;
Best Local Similarity 89.8%; Pred. No. 1.1e-41;
Matches 106; Conservative 1; Mismatches 2; Indels 9; Gaps 5;
;;
QY 103 DSNPRGVSAVLSRSPDP-LFIRKSPITTCLVVDLAPSKGTVNLWTSRAS---GKPVNHS 158
DB 2 DSNPRGVSAVLSRSPDXLFIRKSPITTCLVVDLAPSKGTVNLWTSRXXSXKGPVNH 61
DB 62 TRREKQRXNXXGTLVTVSTLPVGTWIEGET-QCRVTHPLRALXMRSTYTSGP 118
;;
RESULT 14
US-08-646-981-16
;; Sequence 16, Application US/08646981
;; Patent No. 5852183
;; GENERAL INFORMATION:
;; APPLICANT: MAEDA, HIROAKI
;; APPLICANT: EDA, YASUYUKI
;; APPLICANT: KIMACHI, KAZUHIKO
;; APPLICANT: ONO, YOICHI
;; APPLICANT: TOKIYOSHI, SACHIO
;; TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
;; TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
;; STREET: PO BOX 747
;; CITY: FALLS CHURCH
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22040-0747
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/646,981
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WEINER, MARC S
;; REGISTRATION NUMBER: 32,181
;; REFERENCE/DOCKET NUMBER: 1488-106
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 334 amino acids

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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:52:29 ; Search time 32.9929 Seconds
(without alignments)
1657.949 Million cell updates/sec

Title: US-09-847-208B-7
Perfect score: 3060
Sequence: 1 EPKSCDKTHTPCPCPAPELL.....HEAAPSQTQVQRAVSNPGK 569

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|--------|--------------------|--------------|---------------------|
| 1 | 1766 | 57.7 | 428 1 EHHU | Ig epsilon chain C |
| 2 | 1705.5 | 55.7 | 426 2 I36948 | Ig epsilon chain C |
| 3 | 1225 | 40.0 | 330 1 GHU | Ig gamma-1 chain C |
| 4 | 1219 | 39.8 | 374 2 S69339 | Ig heavy chain V r |
| 5 | 1217 | 39.8 | 255 4 S31866 | Ig gamma-1 chain C |
| 6 | 1172 | 38.3 | 234 2 PT0207 | Ig gamma chain C r |
| 7 | 1138 | 37.2 | 377 2 A23511 | Ig gamma-3 chain C |
| 8 | 1136 | 37.1 | 289 1 A60764 | Ig gamma-3 chain C |
| 9 | 1123 | 36.7 | 289 1 G3HWT | Ig gamma-3 chain C |
| 10 | 1107 | 36.2 | 326 1 G4HU | Ig gamma-2 chain C |
| 11 | 1097 | 35.8 | 327 1 G4HU | Ig gamma-4 chain C |
| 12 | 883 | 28.9 | 323 1 GHRB | Ig gamma chain C r |
| 13 | 868.5 | 28.4 | 328 2 I47160 | Ig gamma 2b chain |
| 14 | 868.5 | 28.4 | 328 2 I47159 | Ig gamma 2b chain |
| 15 | 865 | 28.3 | 277 2 I47162 | Ig gamma 2a chain |
| 16 | 862.5 | 28.2 | 429 1 EHRT | Ig epsilon chain C |
| 17 | 858 | 28.0 | 329 1 G2GP | Ig gamma-2 chain C |
| 18 | 847.5 | 27.7 | 328 2 I47158 | Ig gamma 1 chain C |
| 19 | 840.5 | 27.5 | 328 2 I47161 | Ig gamma 3 chain C |
| 20 | 834.5 | 27.3 | 548 2 S38864 | Ig epsilon chain C |
| 21 | 820 | 26.8 | 470 2 S22080 | Ig heavy chain pre |
| 22 | 813 | 26.6 | 333 2 P50018 | Ig gamma-2b chain |
| 23 | 812.5 | 26.6 | 329 1 G3MSC | Ig gamma-3 chain C |
| 24 | 811.5 | 26.5 | 308 2 C30554 | Ig heavy chain C r |
| 25 | 811.5 | 26.5 | 472 2 S31459 | Ig gamma-1 chain C |
| 26 | 801.5 | 26.2 | 398 1 G3MSM | Ig gamma-3 chain C |
| 27 | 794.5 | 26.0 | 444 2 PC4436 | monoclonal antibody |
| 28 | 789.5 | 25.8 | 324 1 GLMS | Ig gamma-1 chain C |
| 29 | 784.5 | 25.6 | 326 2 P50017 | Ig gamma-1 chain C |

| | | | | |
|----|-------|------|--------------|--------------------|
| 30 | 784.5 | 25.6 | 393 1 G1MSM | Ig gamma-1 chain C |
| 31 | 776.5 | 25.4 | 329 2 S00847 | Ig gamma-2c chain |
| 32 | 776 | 25.4 | 330 1 G2MSA | Ig gamma-2a chain |
| 33 | 776 | 25.4 | 469 2 S37483 | Ig gamma-2a chain |
| 34 | 772 | 25.2 | 335 1 G2MSAB | Ig gamma-2a chain |
| 35 | 771 | 25.2 | 339 1 G2MSAM | Ig gamma-2a chain |
| 36 | 766.5 | 25.0 | 388 1 EHMS | Ig epsilon chain C |
| 37 | 761 | 24.9 | 446 2 S40295 | Ig gamma-2a chain |
| 38 | 751.5 | 24.6 | 474 1 G2MS11 | Ig gamma-2b chain |
| 39 | 750 | 24.5 | 423 1 EHMS5 | Ig epsilon chain C |
| 40 | 747.5 | 24.4 | 322 2 P50019 | Ig gamma-2a chain |
| 41 | 746.5 | 24.4 | 405 1 G2MSBM | Ig gamma-2b chain |
| 42 | 735 | 24.0 | 327 2 S06611 | Ig gamma-2 chain C |
| 43 | 731.5 | 23.9 | 475 2 S01321 | Ig gamma-2b chain |
| 44 | 669 | 21.9 | 180 2 I46732 | Ig gamma heavy cha |
| 45 | 576 | 18.8 | 227 2 PH1215 | Ig epsilon chain C |

ALIGNMENTS

RESULT 1

EHHU
Ig epsilon chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C:Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116;
R:Flanagan, J.C.; Rabbitts, T.H.
EMBO J. 1, 655-660, 1982
A>Title: The sequence of a human immunoglobulin epsilon heavy chain constant region 9
A:Reference number: A22771; MUID:84236029; PMID:6234164
A:Accession: A22771
A:Molecule type: DNA
A:Residues: 1-428 <FLA>
A:Cross-references: GB:L00022; GB:V00555; NID:g185035
R:Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
A>Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseu
A:Reference number: A23195; MUID:84207910; PMID:6327276
A:Accession: A23195
A:Molecule type: DNA
A:Residues: 2-428 <UED>
A:Cross-references: GB:J00222; NID:g184755
R:Zhang, K.; Saxton, A.; Max, E.E.
J. Exp. Med. 176, 233-243, 1992
A>Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splic
A:Reference number: PH1214; MUID:92308839; PMID:1613458
A:Accession: PH1214
A:Molecule type: DNA
A:Residues: 320-428 <ZHA>
A:Cross-references: EMBL:X63693; GB:S38668; NID:g32987
R:Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; S
Nucleic Acids Res. 11, 719-726, 1983
A>Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon
A:Reference number: A93491; MUID:83168897; PMID:6300763
A:Accession: A93491
A:Molecule type: mRNA
A:Residues: 1-428 <SEN>
A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035
R:Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.
Cell 29, 691-699, 1982
A>Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A:Reference number: A90824; MUID:83001945; PMID:6288268
A:Accession: A90824
A:Molecule type: DNA
A:Residues: 1-358, 'L', 360-428 <MAX>
A:Cross-references: GB:J00222; NID:g184755
A>Note: This sequence difference may be due to polymorphism
R:Benich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
In Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.
A:Reference number: A94418
A:Accession: A94418
A:Molecule type: protein

A:Residues: 'GAWTL',6,'X',8-16,'B',18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L',124
A:Experimental source: myeloma protein Nd
R:Kerten, J.H.; Molgaard,H.V.; Houghton, M.; Darbyshire, R.B.; Vinay, J.; Bell, L.O.; G
A:Title: Cloning and sequence determination of the gene for the human immunoglobulin epsilon
A:Reference number: A93933; MUID:83065234; PMID:6815656
A:Accession: B93933
A:Molecule type: mRNA
A:Residues: 1-40:68-114;427-428 <KEN>
A:Cross-references: GB:L00022; NID:g185035
R:Ikemura, S
FEBS Lett. 224, 306-310, 1987
A:Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragment
A:Reference number: S02438; MUID:88083554; PMID:3121387
A:Accession: S02438
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 98-352 <IKE>
R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
A:Reference number: A53116; MUID:94103254; PMID:8276835
A:Accession: A53116
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 320-428 <ZH2>
A:Experimental source: myeloma U266-derived cell line AF-10
A:Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
R:Hellman, L.
Eur. J. Immunol. 23, 159-167, 1993
A:Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of
A:Reference number: A46536; MUID:93122085; PMID:8419166
A:Accession: C46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 382-426 <HEL>
A:Cross-references: GB:S55273; NID:g263166; PIDN:AMB24857.1; PID:g263167
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:125297)
A:Accession: D46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 382-391 <HE2>
A:Cross-references: GB:S55276; NID:g263168; PIDN:AMB24858.1; PID:g263169
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:125299)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
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A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AMB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA

```

Matches 347: Conservative 17; Mismatches 57; Indels 24; Gaps 7;
OY 129 REPQVYTLPRSRDELTKNQVSLT--CLVKGYPYSDIAVENESNQPENNYKTPR-PVLDS 185
Db 4 QSPSVPFLTRCKCKNIPSNATSVTLGCLATGFPEPVVMTWT-GSLANGTMTLPAATLTL 62
OY 186 VGSEFLVSKLVNDRSRMOQGVFCSQVMEALHNHY-QORSLSPGKVEGGSGSGGS 244
Db 63 SGHVAITSLTLV-SGAMAK-QMFTCRVAHPTSSIDWDNKKFYSVC----- 105
OY 245 GGGGSFPPRYKIIQSSCDGGGHPPTIQLCLVSGYTPGTINTITWLEDGVMDVLSTA 304
Db 106 --SRDFFPPRYKIIQSSCDGGGHPPTIQLCLVSGYTPGTINTITWLEDGVMDVLSTA 163
OY 305 STTQEGELASTQSELTLSQKHWLSDRYTCQVTVQGHFFEDSTKKCADSNRGVSATLSR 364
Db 164 STTQEGELASTQSELTLSQKHWLSDRYTCQVTVQGHFFEDSTKKCADSNRGVSATLSR 223
OY 365 PSPDPLFRKSPITTCCLVVDLAPSKGYNLTWSPASGKPVNHSTRKEKQNGTLVTST 424
Db 224 PSPDPLFRKSPITTCCLVVDLAPSKGYNLTWSPASGKPVNHSTRKEKQNGTLVTST 283
OY 425 LPVGRDMIESETQCRTVHPHLRALMRSTTKTSGPRAAEVVAFAFAPMPGSRDRTL 484
Db 284 LPVGRDMIESETQCRTVHPHLRALMRSTTKTSGPRAAEVVAFAFAPMPGSRDRTL 343
OY 485 ACLIQNFWPEDIISQVWLHNEYOLDPARHSTTPQPKTKSGGFVPSRLVETRAEQRDEF 544
Db 344 ACLIQNFWPEDIISQVWLHNEYOLDPARHSTTPQPKTKSGGFVPSRLVETRAEQRDEF 403
OY 545 ICRAVHEAASPSQTVQRAVSYPNGK 569
Db 404 ICRAVHEAASPSQTVQRAVSYPNGK 428

RESULT 2
136948
Ig epsilon-chain - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C:Accession: J36948
R:Sakoyama, Y.; Hong, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A:Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orang
A:Reference numbers: J36948; MUID:87147196; PMID:3103123
A:Accession: J36948
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-426 <RES>
A:Cross-references: GB:M15398; NID:g176797; PIDN:AAA5416.1; PID:g176798
C:Genetics:
A:Introns: 103/1; 209/1; 317/1
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
F:J36-405/Domain: immunoglobulin homology <IM>

Query Match 55.7%; Score 1705.5; DB 2; Length 426;
Best Local Similarity 76.0%; Pred. No.1.3e-98;
Matches 338; Conservative 20; Mismatches 62; Indels 25; Gaps 8;
OY 129 REPQVYTLPRSRDELTKNQVSLT--CLVKGYPYSDIAVENESNQPENNYKTPR-PVLDS 185
Db 3 RSPSLFPLTRCKCKNIPSNATSVTLGCLAMGYFPEPVMTWDA-GSLNGTMTLPAATLTLTP 61
OY 186 VGSEFLVSKLVNDRSRMOQGVFCSQVMEALHNHY-QORSLSPGKVEGGSGSGGS 244
Db 62 SGHVAITSLTLV-SGAMAK-QMFTCRVAHPTSSIDWDNKKFYSVC----- 104
OY 245 GGGGSFPPRYKIIQSSCDGGGHPPTIQLCLVSGYTPGTINTITWLEDGVMDVLSTA 304
Db 105 --SRDFFPPRYKIIQSSCDGGGHPPTIQLCLVSGYTPGTINTITWLEDGVMDVLSTA 161
OY 305 STTQEGELASTQSELTLSQKHWLSDRYTCQVTVQGHFFEDSTKKCADSNRGVSATLSR 364
Db 164 STTQEGELASTQSELTLSQKHWLSDRYTCQVTVQGHFFEDSTKKCADSNRGVSATLSR 223

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Db 162 SATOGEELASTQSELTLSSOKHMLSDRTYTCOVITYOGGFEDSTFKCADSNRGVSAVLSR 221
QY 365 PSEPDLFIRKSPITTLCLVVDLPAPSKGTGNLTWMSRASKGPNVHSTRKEKORNGTLTYST 424
Db 222 PSEPDLFIRKSPITTLCLVVDLPAPSKGTGNLTWMSRASKGPNVHSTRKEKORNGTLTYST 281
QY 425 LPVGTDMISEGYQCVHTPHLPRLALMRSTTKSGPRAPEVAFATPEPGRDRTL 484
Db 282 LPVGTDMISEGYQCVHTPHLPRLALMRSTTKSGPRAPEVAFATPEPGRDRTL 341
QY 485 ACLIONMPEDISVQWLNHEVQLPDARHSTTPPKTKSGFVFVSRLVTRAEWQDEF 544
Db 342 ACLIONMPEDISVQWLNHEVQLPDARHSTTPPKTKSGFVFVSRLVTRAEWQDEF 401
QY 545 ICRVHEAASPQTVORAVSNPCK 569
Db 402 ICRVHEAASPQTVORAVSNPCK 426

RESULT 3
GHHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C:Accession: A93433; S36861; S33887; B90563; A90564; B91688; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <EHL>
A:Cross-references: EMBL:Z17370
A:Note: this sequence has the Gln(17) allelotypic marker, 97-Lys, and the Gln(1) markers, R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obara, M.; Nixkaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943; PMID:6811139
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113/235-330 <TAK>
A:Cross-references: EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, G.M.
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A:Reference number: A90563; MUID:71064024; PMID:5489771
A:Accession: B90563
A:Contents: myeloma protein Eu
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-135 <GUN>
A:Note: this sequence has the Gln(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
A:Reference number: A90564; MUID:71064025; PMID:5530842
A:Accession: A90564
A:Contents: protein
A:Molecule type: protein
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
A:Note: this sequence has the Gln(non-1) markers, 239-Gln and 241-Met
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nle),
igen Primerstruktur.
A:Reference number: A91668; MUID:77070269; PMID:826475

A:Contents: myeloma protein Nle
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E',
A:Note: this sequence has the Gln(17) and Gln(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primerstruktur des kristallisierten monoklonalen Immunglobulins IgG1
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KOL, disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <
A:Note: this sequence has the Gln(3) and Gln(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunog
endriamide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/L: 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83, 144-204, 250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109, 112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 40.0%; Score 1225; DB 1; Length 330;
Best Local Similarity 97.0%; Pred. NO. 6.3e-69;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHGPCPCAPRLDGGPSVFLFPPKPKDTLMSRPETVCVVVDVSHEDPEVK 60
Db 99 EPKSCDKTHGPCPCAPRLDGGPSVFLFPPKPKDTLMSRPETVCVVVDVSHEDPEVK 158
QY 61 NMVYDGVVHNAKTRPREQYNSYTRVSVLTVLHOMMNGKRYKSNKALPAPEKT 120
Db 159 NMVYDGVVHNAKTRPREQYNSYTRVSVLTVLHOMMNGKRYKSNKALPAPEKT 218
QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTP 180
Db 219 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTP 278
QY 181 PVLDSVGSFFLYSLKTLVTKSRMQGCVNVCSCVMEHALLNHYQQRSLSPGK 232
Db 279 PVLDSVGSFFLYSLKTLVTKSRMQGCVNVCSCVMEHALLNHYQQRSLSPGK 330

RESULT 4
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamilchi, A.A.; Aucoeur, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687; PMID:7744049

A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamlich, A.A.
Submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: Immunoglobulin C region; immunoglobulin homology

Query Match 39.8%; Score 1219; DB 2; Length 374;
Best Local Similarity 96.1%; Pred. No. 1,7e-68;
Matches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKDITLMSRTPEVTCVAVDVSHEDPEVKF 60
DB 143 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKDITLMSRTPEVTCVAVDVSHEDPEVKF 202
QY 61 NMVVDGVEVHNATKPREEOYNSTYRVSVLTVLHQMNGKEKCKVSKALPAPIEKT 120
DB 203 NMVVDGVEVHNATKPREEOYNSTYRVSVLTVLHQMNGKEKCKVSKALPAPIEKT 262
QY 121 ISKAKVQPREQYTYLPPSDDELTKNOVSLTCLVKGFPSDIAVEMWNSQPENNKTTTP 180
DB 263 ISKAKGPREQYTYLPPSDDELTKNOVSLTCLVKGFPSDIAVEMWNSQPENNKTTTP 322
QY 181 PVLDSDGSFFLYSKLTVDKSRMOGQNVFSCSVHMEALHNNHYOQRSLSPGK 232
DB 323 PVLDSDGSFFLYSKLTVDKSRMOGQNVFSCSVHMEALHNNHYOQRSLSPGK 374

RESULT 5
S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in *Escherichia coli*
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filipula, D.
Submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products.
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FIL>
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: Immunoglobulin
F:1-22/Region: *Escherichia coli* outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 39.8%; Score 1217; DB 4; Length 255;
Best Local Similarity 96.6%; Pred. No. 1,4e-68;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKDITLMSRTPEVTCVAVDVSHEDPEVKF 60
DB 24 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKDITLMSRTPEVTCVAVDVSHEDPEVKF 83
QY 61 NMVVDGVEVHNATKPREEOYNSTYRVSVLTVLHQMNGKEKCKVSKALPAPIEKT 120
DB 84 NMVVDGVEVHNATKPREEOYNSTYRVSVLTVLHQMNGKEKCKVSKALPAPIEKT 143
QY 121 ISKAKVQPREQYTYLPPSDDELTKNOVSLTCLVKGFPSDIAVEMWNSQPENNKTTTP 180
DB 144 ISKAKGPREQYTYLPPSDDELTKNOVSLTCLVKGFPSDIAVEMWNSQPENNKTTTP 203
QY 181 PVLDSDGSFFLYSKLTVDKSRMOGQNVFSCSVHMEALHNNHYOQRSLSPGK 232

DB 204 PVLDSDGSFFLYSKLTVDKSRMOGQNVFSCSVHMEALHNNHYOQRSLSPGK 255

RESULT 6
PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R:Enllich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716; PMID:2062315
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 38.3%; Score 1172; DB 2; Length 234;
Best Local Similarity 95.6%; Pred. No. 8e-66;
Matches 215; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKDITLMSRTPEVTCVAVDVSHEDPEVKF 60
DB 10 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKDITLMSRTPEVTCVAVDVSHEDPEVKF 69
QY 61 NMVVDGVEVHNATKPREEOYNSTYRVSVLTVLHQMNGKEKCKVSKALPAPIEKT 120
DB 70 NMVVDGVEVHNATKPREEOYNSTYRVSVLTVLHQMNGKEKCKVSKALPAPIEKT 129
QY 121 ISKAKVQPREQYTYLPPSDDELTKNOVSLTCLVKGFPSDIAVEMWNSQPENNKTTTP 180
DB 130 ISKAKGPREQYTYLPPSDDELTKNOVSLTCLVKGFPSDIAVEMWNSQPENNKTTTP 189
QY 181 PVLDSDGSFFLYSKLTVDKSRMOGQNVFSCSVHMEALHNNHYOQRSLSPGK 225
DB 190 PVLDSDGSFFLYSKLTVDKSRMOGQNVFSCSVHMEALHNNHYOQRSLSPGK 234

RESULT 7
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene.
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Insertions: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 37.2%; Score 1138; DB 2; Length 377;
Best Local Similarity 89.7%; Pred. No. 1,9e-63;
Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKDITLMSRTPEVTCVAVDVSHEDPEVKF 60
DB 146 EPKSCDKTHPCPCPAPPELLGSPSVFLPPPKDITLMSRTPEVTCVAVDVSHEDPEVKF 205
QY 61 NMVVDGVEVHNATKPREEOYNSTYRVSVLTVLHQMNGKEKCKVSKALPAPIEKT 120


```

Db      206 KMYVDGVEVHNAAKTRPREQYNSTFRVSVLTVLHODLNGKEYCKVSNKALPAPIEKT 265
      121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 180
      266 ISKTKGQPREPOVYTLPPSRDEMTKNQVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 325
Qy      181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALHNHQOQSLSPGK 232
      326 PVLDSGSEFFLYSKLTVDKSRWQGNVFSQVMEHALHNHQOQSLSPGK 377

```

RESULT 8

```

A: gamma-3 chain C region, form IAT - human
A:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IIM>

```

```

Query Match      37.1%; Score 1136; DB 2; Length 377;
Best Local Similarity 89.7%; Pred. No. 2.5e-63;
Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy      1 EPKSCDTHTCPPCPAPRLGSPVFLPFPKPKDTLMSRPEVTCVAVDVSHEDPEVKF 60
      146 EPKSCDTPPPCPAPRLGSPVFLPFPKPKDTLMSRPEVTCVAVDVSHEDPEVKF 205
      61 NMVYDGVVHNAAKTRPREQYNSTFRVSVLTVLHODLNGKEYCKVSNKALPAPIEKT 120
      206 KMYVDGVEVHNAAKTRPREQYNSTFRVSVLTVLHODLNGKEYCKVSNKALPAPIEKT 265
      121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 180
      266 ISKTKGQPREPOVYTLPPSRDEMTKNQVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 325
Qy      181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALHNHQOQSLSPGK 232
      326 PVLDSGSEFFLYSKLTVDKSRWQGNVFSQVMEHALHNHQOQSLSPGK 377

```

RESULT 9

```

G3HWTI
A: gamma-3 heavy chain disease proteins - human
A:Species: Homo sapiens (man)
C:Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C:Accession: A90442; A92219; A93915; A02149
R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-
A:Reference number: A90442; MUID:81021548; PMID:6774747
A:Accession: A90442
A:Molecule type: protein
A:Residues: 1-289 <FRA>
A:Note: The molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A:Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 cc
A:Note: the sequence of residues 42-76 was taken from the reference that follows
R:Michaelson, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
A:Reference number: A92219; MUID:77118561; PMID:402363
A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W

```

```

A:Accession: A92219
A:Molecule type: protein
A:Residues: 12-97 <MTC>
A:Note: the hinge region in gamma-3 chains is about four times as long as in other ga
      ldu segment (12-28)
A:Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form in
      Rwohlfeinstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
      Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of t
A:Reference number: A90198; MUID:77021516; PMID:823945
A:Contents: heavy chain disease protein ZUC, partial sequence corresponding to residu
A:Accession: A90198
A:Molecule type: protein
A:Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A:Note: this protein lacks most of the V region, all of the CH1 region, and part of t
      R:Alexander, A.; Stelmets, M.; Barilauf, D.; Frangione, B.; Franklin, E.C.; Hood,
      Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A:Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deleti
A:Reference number: A93915; MUID:82247835; PMID:6808505
A:Contents: heavy chain disease protein Omn
A:Accession: A93915
A:Molecule type: mRNA
A:Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-
A:Note: a carboxyl-terminal Lys is removed posttranslationally
A:Note: this sequence may represent an allelic form or another gamma chain subclass
C:Comment: The heavy chain disease protein W is shown.
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339, OMTM:147120
A:Map position: 14q32.33-14q32.33
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglytamic acid
F:203-270/Domain: immunoglobulin homology <IIM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6/40/Binding site: carbonylurate (Asn) (covalent) #status experimental

```

```

Query Match      36.7%; Score 1123; DB 1; Length 289;
Best Local Similarity 88.3%; Pred. No. 1.1e-62;
Matches 204; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy      1 EPKSCDTHTCPPCPAPRLGSPVFLPFPKPKDTLMSRPEVTCVAVDVSHEDPEVKF 60
      59 EPKSCDTPPPCPAPRLGSPVFLPFPKPKDTLMSRPEVTCVAVDVSHEDPEVKF 118
      61 NMVYDGVVHNAAKTRPREQYNSTFRVSVLTVLHODLNGKEYCKVSNKALPAPIEKT 120
      119 KMYVDGVEVHNAAKTRPREQYNSTFRVSVLTVLHODLNGKEYCKVSNKALPAPIEKT 178
      121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 180
      179 ISKTKGQPREPOVYTLPPSRDEMTKNQVSLTCLVKGFPSPDIAYEWESNGOPENNYKTTT 238

```

```

Qy      181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALHNHQOQSLSPG 231
      239 PVLDSGSEFFLYSKLTVDKSRWQGNVFSQVMEHALHNHQOQSLSPG 289

```

RESULT 10

```

G2HU
A: gamma-2 chain C region - human
A:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L. U.S.A. 79, 1984-1988, 1982
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: GB:V00554; GB:J00230; NID:933759; PIDN:CA858438.1; PID:96066056
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.

```



```

A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-1 haplo
A:Reference number: A91749; MUID:84030930; PMID:6313520
A:Molecule type: mRNA
A:Residues: 1-323 <BR>
A:Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R:Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobul
A:Reference number: A90290; MUID:76135469; PMID:1243651
A:Accession: A90290
A:Molecule type: protein
A:Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>
R:Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A:Title: Heavy chain genes of rabbit IgG: Isolation of a cDNA encoding gamma heavy chain
A:Reference number: A93928; MUID:83299917; PMID:6193512
A:Accession: A93928
A:Molecule type: mRNA
A:Residues: 88-103, 'W', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A:Cross-references: GB:M6426; NID:g16511; PIND:AAA31289.1; PID:g165112
A:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker
R:Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin
A:Reference number: A90245; MUID:70110015; PMID:5461106
A:Accession: A90245
A:Molecule type: protein
A:Residues: 132-143, 'E', 145-161 <FRU>
R:Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,
A:Reference number: A94416
A:Accession: A94416
A:Molecule type: Protein
A:Residues: 129-131, 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q',
A:Note: this has the e15 allotypic marker, 185-Ala
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into Ia
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-82/Domain: immunoglobulin homology <IM1>
F:130-199/Domain: immunoglobulin homology <IM2>
F:236-303/Domain: immunoglobulin homology <IM3>
F:113/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 28.9%; Score 883; DB 1; Length 323;
Best Local Similarity 64.5%; Pred. No. 1e-7;
Matches 160; Conservative 34; Mismatches 38; Indels 16; Gaps 2;

QY 1 EPKSCDTH-----TC--PPCPAPILGGSVFLPPPKDTLMSRPEV 44
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 76 QPVCNVAHPATNTKVDKTVAPSTCSKPTCPPELGLGSPVFIEPPKDKTLMISRPV 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 45 TCVVVDVSDHEPEYKFMKYVDGVENHNKTPREEDQNSITRYVSVLTVLHQNMGKEY 104
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 TCVVVDVSDDEPEQVFTWYINNEQVFTAPRLRQOQFNSTIRVYSTPLTHQDWLKEF 195
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 105 KCKVSNKALPAPIEKTTSKAKVOPREPOVYLPRESBELTKNGVSLCLVNGFYPSDIAY 164
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 196 KCKVHNKALPAPIEKTTSKAKGQPLERKVTYIMGPPREELSSRSVSLTCMINGFTPSDISV 255
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 165 EWSNGGPENNYKTTTPYLVDSVGSFFLYSKTLVDKSRMOQGNVSGVMEDALNNHYQOR 224
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 256 EWEKNGKADENYKTTTPAVLDSGVSFLYLNKLSVPTSEMQRQDVFVTCVMEDALNNHYQK 315
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 225 SLSLSPGK 232
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 316 SISRSPPK 323
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESUL.T 13
147160
1g gamma 2b chain constant region - pig (fragment)

```

[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:47:19 ; Search time 17.7654 Seconds

(without alignments)
1328.428 Million cell updates/sec

Title: US-09-847-208B-7

Perfect score: 3060

Sequence: 1 EPKSCDKHTPCPCPAPELL.....HEAASPSQTVQRAVSVPNGK 569

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1766 | 57.7 | 428 | 1 | EPC_HUMAN |
| 2 | 1225 | 40.0 | 330 | 1 | GCI_HUMAN |
| 3 | 1128 | 36.9 | 290 | 1 | GC3_HUMAN |
| 4 | 1107 | 36.2 | 326 | 1 | GC2_HUMAN |
| 5 | 1097 | 35.8 | 327 | 1 | GC4_HUMAN |
| 6 | 883 | 28.9 | 323 | 1 | GC_RABIT |
| 7 | 862.5 | 28.2 | 429 | 1 | EPC_RAT |
| 8 | 858 | 28.0 | 329 | 1 | GC2_CAVPO |
| 9 | 826 | 27.0 | 421 | 1 | EPC_MOUSE |
| 10 | 813 | 26.6 | 333 | 1 | GC_RAT |
| 11 | 812.5 | 26.6 | 329 | 1 | GC3_MOUSE |
| 12 | 801.5 | 26.2 | 398 | 1 | GC3_MOUSE |
| 13 | 789.5 | 25.8 | 324 | 1 | GCI_MOUSE |
| 14 | 784.5 | 25.6 | 326 | 1 | GCI_MOUSE |
| 15 | 784.5 | 25.6 | 393 | 1 | GCIM_MOUSE |
| 16 | 776.5 | 25.4 | 329 | 1 | GC_RAT |
| 17 | 776 | 25.4 | 330 | 1 | GCAB_MOUSE |
| 18 | 772 | 25.2 | 335 | 1 | GCAB_MOUSE |
| 19 | 771 | 25.2 | 399 | 1 | GCAB_MOUSE |
| 20 | 751.5 | 24.6 | 336 | 1 | GCB_MOUSE |
| 21 | 747.5 | 24.4 | 322 | 1 | GC_RAT |
| 22 | 746.5 | 24.4 | 405 | 1 | GCBM_MOUSE |
| 23 | 488.5 | 16.0 | 455 | 1 | MUC_MOUSE |
| 24 | 479.5 | 15.7 | 476 | 1 | MUC_MOUSE |
| 25 | 463.5 | 15.1 | 454 | 1 | MUC_MOUSE |
| 26 | 461 | 15.1 | 458 | 1 | MUC_MOUSE |
| 27 | 452 | 14.8 | 479 | 1 | MUC_MOUSE |
| 28 | 443.5 | 14.5 | 457 | 1 | MUC_MOUSE |
| 29 | 436.5 | 14.3 | 454 | 1 | MUC_MOUSE |
| 30 | 427 | 14.0 | 450 | 1 | MUC_MOUSE |
| 31 | 410 | 13.4 | 391 | 1 | MUC_MOUSE |
| 32 | 391 | 12.8 | 438 | 1 | MUC_MOUSE |
| 33 | 382 | 12.5 | 461 | 1 | MUC_MOUSE |

| | | | | | | |
|----|-------|------|------|---|------------|--------------------|
| 34 | 373 | 12.2 | 438 | 1 | HVC2_HETFR | P23085 heterodontu |
| 35 | 355 | 11.6 | 446 | 1 | MUC_CHICK | P01875 gallus gall |
| 36 | 347 | 11.3 | 340 | 1 | ALC2_HUMAN | P01877 homo sapien |
| 37 | 339.5 | 11.1 | 393 | 1 | HVC3_HETFR | P23086 heterodontu |
| 38 | 334.5 | 10.9 | 353 | 1 | ALC1_HUMAN | P01876 homo sapien |
| 39 | 326 | 10.7 | 353 | 1 | ALC1_GORGO | P20758 gorilla gor |
| 40 | 308 | 10.1 | 370 | 1 | HVC1_HETFR | P23084 heterodontu |
| 41 | 303 | 9.9 | 344 | 1 | ALC_MOUSE | P01878 mus musculu |
| 42 | 293.5 | 9.6 | 299 | 1 | ALC_MOUSE | P01879 oryctolagus |
| 43 | 254 | 8.3 | 481 | 1 | MUC_MOUSE | P23735 ictalurus p |
| 44 | 229 | 7.3 | 383 | 1 | DTC_HUMAN | P01880 homo sapien |
| 45 | 179 | 5.8 | 1242 | 1 | NPHN_MOUSE | Q9qzsf mus musculu |

ALIGNMENTS

| | | | | | | |
|----------|--|-----------|------|---------|--|--|
| RESULT 1 | | | | | | |
| AC | EPC_HUMAN | STANDARD: | PRT: | 428 AA. | | |
| AC | P01854: | | | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | | | |
| DT | 15-JUN-2002 (Rel. 41, Last annotation update) | | | | | |
| DE | Ig epsilon chain C region. | | | | | |
| GN | IGHF. | | | | | |
| OS | Homo sapiens (Human). | | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | | |
| OX | NCBI_TaxID=9606; | | | | | |
| RN | [1] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RX | MEDLINE=83168897; PubMed=6300763; | | | | | |
| RA | Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K., | | | | | |
| RA | Kikuchi M., Sugino Y., Nishida Y., Honjo T.; | | | | | |
| RT | "Molecular cloning and nucleotide sequencing of human immunoglobulin | | | | | |
| RT | epsilon chain cDNA."; | | | | | |
| RL | Nucleic Acids Res. 11:719-726(1983). | | | | | |
| RN | [2] | | | | | |
| RP | SEQUENCE FROM N.A., AND VARIANT LEU-359. | | | | | |
| RX | MEDLINE=83001945; PubMed=6288268; | | | | | |
| RA | Max E.E., Batley J., Ney R., Kirsch I.R., Leder P.; | | | | | |
| RT | "Duplication and deletion in the human immunoglobulin epsilon genes."; | | | | | |
| RT | Cell 29:691-699(1982). | | | | | |
| RN | [3] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RX | MEDLINE=84236029; PubMed=6234164; | | | | | |
| RA | Flanagan J.G., Rabbits T.H.; | | | | | |
| RT | "The sequence of a human immunoglobulin epsilon heavy chain constant | | | | | |
| RT | region gene, and evidence for three non-allelic genes."; | | | | | |
| RL | EMBO J. 1:655-660(1982). | | | | | |
| RN | [4] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RX | MEDLINE=84207910; PubMed=6327276; | | | | | |
| RA | Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.; | | | | | |
| RT | "Long terminal repeat-like elements flank a human immunoglobulin | | | | | |
| RT | epsilon pseudogene that lacks introns."; | | | | | |
| RL | EMBO J. 1:1539-1544(1982). | | | | | |
| RN | [5] | | | | | |
| RP | PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND). | | | | | |
| RA | Benich H.H., Johansson S.G.O., von Bahr-Lindstrom H.; | | | | | |
| RT | (In) Bach M.K. (eds.); | | | | | |
| RT | Immediate hypersensitivity: modern concepts and developments, pp.1-36, | | | | | |
| RL | Marcel Dekker, New York (1978). | | | | | |
| RN | [6] | | | | | |
| RP | SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A. | | | | | |
| RX | MEDLINE=83065234; PubMed=6815656; | | | | | |
| RA | Kenlen J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J., | | | | | |
| RA | Bell L.O., Gould H.J.; | | | | | |
| RT | "Cloning and sequence determination of the gene for the human | | | | | |
| RT | immunoglobulin epsilon chain expressed in a myeloma cell line."; | | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982). | | | | | |
| RN | [7] | | | | | |

```

RP      3D-STRUCTURE MODELING.
RX      MEDLINE=87089648; PubMed=3796618;
RA      Padian E.A., Davies D.R.;
RL      "A model of the Fc of Immunoglobulin E.";
CC      Mol. Immunol. 23:1063-1075(1986).
-----
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CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC      at the European Bioinformatics Institute. There are no restrictions on its
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CC      entities requires a license agreement (See http://www.isdb.ch/announce/
CC      or send an email to license@isb.slb.ch).
DR      EMBL, L00022; AAB59424.1; ALT_INT.
DR      PIR, A02142; EHBU.
DR      PIR, A22771; A22771.
DR      PIR, A23195; A23195.
DR      PDB, IIGE, 15-JUL-92.
DR      Genew: HGNC:5522; IGHE.
DR      MIM, 147180; .
DR      InterPro: IPRO03006; Ig_MHC.
DR      InterPro: IPRO03597; Ig-cl.
DR      Pfam: PF00047; Ig_4.
DR      SMART: SMO0407; IGc1_4.
DR      PROSITE: PS00290; IG_MHC_3.
KW      Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KM      3D-structure.
FT      NON_TER          1           1
FT      DISULFID         14          14    INTERCHAIN (WITH A LIGHT CHAIN).
FT      DISULFID         15          105
FT      DISULFID         29          85
FT      DISULFID        121          121    INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID        135          193
FT      DISULFID        209          209    INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID        239          299
FT      DISULFID        345          405
FT      CARBOHYD         21           21    N-LINKED (GLCNAC. . . ).
FT      CARBOHYD         49           49    N-LINKED (GLCNAC. . . ).
FT      CARBOHYD         99           99    N-LINKED (GLCNAC. . . ).
FT      CARBOHYD        146          146    N-LINKED (GLCNAC. . . ).
FT      CARBOHYD        252          252    N-LINKED (GLCNAC. . . ).
FT      CARBOHYD        275          275    N-LINKED (GLCNAC. . . ).
FT      VARIANT          359           W -> L (POSSIBLE POLYMORPHISM).
FT                                     /FTID-VAR_003885.
SQ      SEQUENCE       428 AA: 47019 MW: 25C4CA072AA55B8A CRC64;
Query Match              57.7%; Score 1766; DB 1; Length 428;
Best Local Similarity   78.0%; Pred. No. 1.7e-114;
Matches 347; Conservative 17; Mismatches 57; Indels 24; Gaps 7;
QY      129 REPVVYTLLPSRDELTKNQSLT--CLVKGFPSPSDIAEVESNGCPENNYKTP-PVYDS 185
DY      :|::||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DY      4 QSPSVFLPTRCKKNIPNSATSVTLGICLATGVFFPEVVMWTWTF-GSLNTGTMTLATITLL 62
QY      186 VGSFELISKLVYDKSRMOCGNVFSCSYNHDLHNHY-QQRSLISPGKVBEVGSGSGGGS 244
DY      |||||:||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DY      63 SGHAIATISLTV-SGAAMK-OIMTCRAVAHPFSSTDWVDNKFKTSYC----- 105
QY      245 GGGSFPPPTVKIILOSCDGCGGHPPPTIQLLCIVSGVPGITINTTWLEDGOVMDVLSTA 304
DY      ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DY      106 --SDPFPPPIKKLIIOSCDCGGHHPPPIQLLCIVLSGVTGITINTTWLEDGOVMDVLSTA 163
QY      305 STTOEGELASTOSSELTIQKHMLSDRYTCQVTVYGHTFEESTPKCADSNRGVSAYLSR 364
DY      ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DY      164 STTOEGELASIQSELTISOXKMWLDRIYTCQVTVYGHTFEESTPKCADSNRGVSAYLSR 223
QY      365 PSPPDLELRKSPTITCYLVDLAPSKGYVNLTWSRASGKPVNASHSTRKEEKORNGLTYVST 424
DY      ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DY      224 PSPPDLELRKSPTITCLEVNDLPAPSKGYVNLTWSRASGKPVNASHSTRKEEKORNGLTYVST 283
QY      425 LPVSTRMISETYQCRTYTHPLRALMRSTTKSGPRAAEYVAFAFEPMPGRDKRTL 484
DY      ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

| | | | |
|----------|---|---|--------------|
| Db | 284 | LPVGRDWTGEGTGYCCRVATHPHPLRALMNSTRTKTSGPRAAPEVYATAPEMPWSRDKRTL | 34.3 |
| Qy | 465 | ACLIQNEFMEDISVGMVLHNEVQLPDARHSTTOPRKTKGSEFFVFSRLVETRAEMQKDER | 544.4 |
| Db | 344 | ACLIQNEFMEDISVGMVLHNEVQLPDARHSTTOPRKTKGSEFFVFSRLVETRAEMQKDER | 403.0 |
| Qy | 545 | ICRAVHEAASPQTVQRAVSNPGK | 569 |
| Db | 404 | ICRAVHEAASPQTVQRAVSNPGK | 428 |
| RESULT 2 | | | |
| | GCL_HUMAN | STANDARD; | PRT; 330 AA. |
| AC | P01857; | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update) | | |
| DE | Ig gamma-1 chain C region. | | |
| GN | IGHG1. | | |
| OS | Homo sapiens (Human). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Euteria; Primates; Catarrhini; Hominiidae; Homo. | | |
| OX | NCBI_TaxID=9606; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | MEDLINE=82274238; PubMed=6287432; | | |
| RA | Ellison J.W., Berson B.J., Hood L.E.; | | |
| RT | "The nucleotide sequence of a human immunoglobulin C gamma1 gene.;" | | |
| RL | Nucleic Acids Res. 10:4071-4079(1982). | | |
| RN | [2] | | |
| RP | SEQUENCE OF 1-135 (MYELOMA PROTEIN EU). | | |
| RA | MEDLINE=71064024; PubMed=5489771; | | |
| RA | Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., | | |
| RA | Waxdal M.J., Edelman G.M.; | | |
| RT | "The covalent structure of a human gamma G-immunoglobulin. VII. Amino | | |
| RL | acid sequence of heavy-chain cyanogen bromide fragments H1-H4.;" | | |
| RL | Biochemistry 9:3161-3170(1970). | | |
| RN | [3] | | |
| RP | SEQUENCE OF 136-329 (EU). | | |
| RA | MEDLINE=71064025; PubMed=5530842; | | |
| RA | Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H., | | |
| RA | Edelman G.M.; | | |
| RT | "The covalent structure of a human gamma G-immunoglobulin. 8. Amino | | |
| RL | acid sequence of heavy-chain cyanogen bromide fragments H3-H7.;" | | |
| RL | Biochemistry 9:3171-3181(1970). | | |
| RN | [4] | | |
| RP | SEQUENCE (MYELOMA PROTEIN NIE). | | |
| RA | MEDLINE=77070269; PubMed=826475; | | |
| RA | Ponstingl H., Hilschmann N.; | | |
| RT | "The role of antibody structure. The primary structure of a | | |
| RT | monoclonal IgG1 immunoglobulin (myeloma protein Nle). III. The | | |
| RT | chymotryptic peptides of the H-chain, alignment of the tryptic | | |
| RT | peptides and discussion of the complete structure.;" | | |
| RL | Hope-seyler's Z. Physiol. Chem. 357:1571-1604(1976). | | |
| RN | [5] | | |
| RP | SEQUENCE (MYELOMA PROTEIN K8). AND DISULFIDE BONDS. | | |
| RA | MEDLINE=83289131; PubMed=6884994; | | |
| RA | Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; | | |
| RT | "Three-dimensional structure determination of antibodies. Primary | | |
| RT | structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.;" | | |
| RL | Hope-seyler's Z. Physiol. Chem. 364:713-747(1983). | | |
| RN | [6] | | |
| RP | DISULFIDE BONDS. | | |
| RA | MEDLINE=71064027; PubMed=4923144; | | |
| RA | Gall W.E., Edelman G.M.; | | |
| RT | "The covalent structure of a human gamma G-immunoglobulin. X. | | |
| RT | intrachain disulfide bonds.;" | | |
| RL | Biochemistry 9:3188-3196(1970). | | |
| RN | [7] | | |
| RP | DISULFIDE BONDS. | | |
| RA | MEDLINE=77070267; PubMed=1002129; | | |
| RA | Dreier L., Schwarz J., Reichel W., Hilschmann N.; | | |

"Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the RT cyanoen bromide cleavage products, and the disulfide bridges." RT Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

[8]

RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).

CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS.
CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.
CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155,166,177,195,198,269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.
CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 198,267&272.

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CC -----

DR EMBL: J00228; AAC82527.1; ALT_INIT.
DR PIR: A02146; GHU.
DR PDB: 1FC1; 15-JUL-92.
DR PDB: 1FC2; 15-JUL-92.
DR Genew: HGNC:5525; IGHL1.
DR MIM: 147100; -
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00410; Ig-like; 1.
DR SMART: SM00407; IGcl; 2.
DR PROSITE: PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; 3D-structure.

KW 3D-structure. 1 1
FT NON_TER 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 223 CH2.
FT DOMAIN 224 330 CH3.
FT DISULFID 27 83 INTERCHAIN (WITH LIGHT CHAIN).
FT DISULFID 103 103 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 144 204 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 250 308
FT CARBOHYD 180 180
FT MOD_RES 330 330
FT VARIANT 97 97
FT VARIANT 239 239
FT VARIANT 241 241
FT STRAND 123 126
FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164
FT STRAND 165 166

FT STRAND 175 178
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 206
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 240
FT TURN 241 242
FT STRAND 245 256
FT STRAND 260 266
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 324
SQ SEQUENCE 330 AA; 36106 MW; 3770BE106C2FA33D CRC64;

Query Match 40.0%; Score 1225; DB 1; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.2e-77;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDTHHCPCPAPBELLGSPVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 60
Db 99 EPKSCDTHHCPCPAPBELLGSPVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 158
QY 61 NMIVDGEVHNHAKTKPREDOYNSTYRVVSVLTVLHQDMNMGKEYCKKCVSKALPAPIEKT 120
Db 159 NMIVDGEVHNHAKTKPREDOYNSTYRVVSVLTVLHQDMNMGKEYCKKCVSKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSBDLTKNOVSLTCLVKGFPSPDAVEMSNQPENNYKTTT 180
Db 219 ISKAKGPREPOVYTLPPSBDLTKNOVSLTCLVKGFPSPDAVEMSNQPENNYKTTT 278
QY 181 PVLDSVGSFPLYSKLTVDKSRWQGNFSCSVMEALHNHYOQKSLSLSPGK 232
Db 279 PVLDSVGSFPLYSKLTVDKSRWQGNFSCSVMEALHNHYOQKSLSLSPGK 330

RESULT 3
GC3_HUMAN
ID GC3_HUMAN STANDARD; PRT; 290 AA.
AC P01860;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN IGHG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP MEDLINE=81021548; PubMed=6774747;
RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RL gamma 3 heavy-chain disease protein wis.";
RN Biochemistry 19:4304-4308(1980).
[2]
RN REVISIONS TO 12-97 (PROTEIN WIS).
RX MEDLINE=77118561; PubMed=402363;
RA Michaelson T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable
quadruplication of a 15-amino acid residue basic unit.";

RL J. Biol. Chem. 252:883-889(1977).
RN [3]
RP REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RA MEDLINE=77021516; PubMed=823945;
RX Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
RZ Structure of the FC fragment of immunoglobulin G3."
RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN [4]
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RA MEDLINE=82247835; PubMed=6808505;
RX Alexander A., Steilmetz M., Barilla D., Frangione B.,
RT Franklin E.C., Hood L., Buxbaum J.N.;
RZ "Gamma Heavy chain disease in man: cDNA sequence supports partial
gene deletion model."
RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC -1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.
CC -1- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WAS IS SHOWN.
CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
REF. 2.
CC -1- MISCELLANEOUS: DISEASE PROTEIN WAS IS LACKING MOST OF THE V REGION
AND ALL OF THE CHI REGION.
CC -1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
GAMMA-3 HEAVY CHAINS.
CC -1- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
OR ANOTHER GAMMA CHAIN SUBCLASS.
CC -1- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
SEGMENT (12-28).

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DR EMBL; J00231; AAA52805.1; ALT_SEQ.
DR PIR; A02149; G3HDWI.
DR HSSP; P01857; 1BC1.
DR Genew; HGNC:3527;IGHG3.
DR MIM; 147120; -
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SMO0410; IG_Like; 1.
DR SMART; SMO0407; Igcl; 1.
DR PROSITE; PS00290; Ig_MHC; 1.
FW Immunoglobulin domain; Immunoglobulin C region; glycoprotein; Repeat.
FT DOMAIN 12 73 HINEE.
FT DOMAIN 74 183 CH2.
FT DOMAIN 184 289 CH3.
FT REPEAT 29 43
FT REPEAT 44 58
FT REPEAT 59 73
FT MOD_RES 1 1
FT CARBOHYD 6 6 PYROLIDONE CARBOXYLIC ACID.
FT DISULFID 7 7 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 24 24 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 27 27 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 33 33 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 39 39 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 42 42 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 48 48 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 54 54 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 57 57 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 63 63 INTERCHAIN (WITH HEAVY CHAIN DIMER).

[illegible]

RA Krawinkel U., Rabbits T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 RT genes";
 RL EMBO J. 1:403-407(1982).
 RN [4]
 RN SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 RT evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]
 RN SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 RT domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RN SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 RT immunoglobulin gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RN REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RN SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 RT immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RN DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RL "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RN Biochem. J. 121:217-225(1971).
 RN [10]
 RN DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
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 CC -----
 CC
 CC EMBL: J00230; AAB59393.1; -
 DR PIR: A02148; G2HD.
 DR HSSP: P01857; 1FC1.
 DR Genew: HGNC:5526; IGHG2.
 DR MIM: 147110; -
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003600; Ig_like.
 DR Pfam: PF00047; Ig_3.
 DR SMART: SM00410; Ig_like; 1.
 DR SMART: SM00407; IGc1; 2.
 DR PROSITE: PS00290; IG_MHC; 2.
 KM Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.

FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT SITE 156 156
 FT MOD_RES 326 326
 FT VARIANT 60 60
 FT CONFLICT 109 109
 FT SEQUENCE 326 AA; 35884 MW; 8310878C687BCF9C CRC64;
 SQ
 Query Match 36.2%; Score 1107; DB 1; Length 326;
 Best Local Similarity 88.4%; Pred. No. 2.9e-69;
 Matches 205; Conservative 12; Mismatches 11; Indels 4; Gaps 2;
 QY 1 EPKSCDKTHCTPCPCAPPELLGSPVFLPPPKKDTLMISRPVTCVVDVSHEDPEYKF 60
 DB 99 ERKCCVE---CPGPCPAPV-VAGPSVFLPPPKDKTLMISRPVTCVVDVSHEDPEYQF 154
 QY 61 NMVYDGVVHNKTKPREQYNSRYRVSVTLVTHQNMNGKREKCKVSNKALPAPTEKT 120
 DB 155 NMVYDGVVHNKTKPREQYNSRYRVSVTLVTHQNMNGKREKCKVSNKALPAPTEKT 214
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTP 180
 DB 215 ISKTKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTP 274
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMHEDALHNHYQKSLSPCK 232
 DB 275 PMLDSGGSFFLYSKLTVDKSRWQGNVFSQVMHEDALHNHYQKSLSPCK 326
 RESULT 5
 G4_HUMAN STANDARD: PRT: 327 AA.
 ID G4_HUMAN
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-4 chain C region.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid:9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=83157104; PubMed=6299662;
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 1:11-18(1981).
 RN [2]
 RN SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE=70207560; PubMed=4192699;
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 RT constant region of a gamma 4 chain.";
 RL Biochem. J. 117:33-47(1970).
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 CC -----

QY 105 KCVSNKALPAPIKTSKAVKPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIV 164
 DB 196 KCKVHNKALPAPIKTSKAVKPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIV 255
 QY 165 EMENSGPENNYKTTTPVLDVSGSFLLSKITVDKSRKQGNVSCSYMHALNHVYOR 224
 DB 256 EMENSGPENNYKTTTPVLDVSGSFLLSKITVDKSRKQGNVSCSYMHALNHVYOR 315
 QY 225 SLSPGK 232
 DB 316 SLSPGK 323

RESULT 7
 EPC_RAT
 ID EPC_RAT STANDARD: PRT: 429 AA.
 AC P01855:
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig epsilon chain C region.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).
 RC STRAIN=100/C/MSL;
 RX MEDLINE=83064537; PubMed=6292865;
 RA Hellman L., Petersson U., Engstrom A., Karlsson T., Bennich H.;
 RT "Structure and evolution of the heavy chain from rat immunoglobulin
 E.";
 RL Nucleic Acids Res. 10:6041-6049(1982).
 RN [2]
 RP SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
 RX MEDLINE=83182019; PubMed=6820340;
 RA Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
 RT "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:
 RT construction, identification, and DNA sequence.";
 RL DNA 1:335-343(1982).
 RN [3]
 RP SEQUENCE OF 205-306 FROM N.A.
 RX MEDLINE=82174576; PubMed=6803238;
 RA Hellman L., Petersson U., Bennich H.;
 RT "Characterization and molecular cloning of the mRNA for the heavy
 RT (epsilon) chain of rat immunoglobulin E.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
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 CC -----
 DR EMBL: J00744; AAA41379.1; ALT_INIT.
 DR PIR: A02143; EHRT.
 DR HSSP: P01854; IIGC.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig_4.
 DR SMART: SM00410; Ig_Like; 3.
 DR SMART: SM00407; IGCL; 1.
 DR PROSITE: PS00290; IG_MHC; 3.
 DR Immunoglobulin domain; Immunoglobulin C region.
 KW NON_TER 1
 FT CONFLICT 168 168 R -> N (IN REF. 2).
 FT CONFLICT 308 308 P -> L (IN REF. 2).
 SQ SEQUENCE 429 AA; 48671 MW; D2970B34EF8A22B0 CRC64;

Query Match

28.2%; Score 862.5; DB 1; Length 429;

Best Local Similarity 40.5%; Pred. No. 2.8e-52;
 Matches 181; Conservative 71; Mismatches 162; Indels 33; Gaps 11;
 QY 126 VQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVAVEMENSGPENNYKTTTPVLDVSGSFLLSKITVDKSRKQGNVSCSYMHALNHVYOR 185
 DB 1 VSKAPSLYENKTPKLTCLVLDL-ESEENITVTWREKKSIGSASORSTKHNMTTITS 272
 QY 186 VGSFELYSKLTVDKSRW-OQGNVSCSYMHALNHVYORSLSPCKVEGGGSGGGS 244
 DB 55 IGSDL--KTTTSQMTSMKSAKNFTCHTH-APSTFVSDLITRRAPVI----- 100
 QY 245 GGGGSPPTPVKLIQSSCGDGGHPPPTQLCLVSGYPTGTTITWL-EDGQVMDVLIST 303
 DB 101 -----TKPTVDLHSSCDPNA-FHSTQLCYFYGHIONDVSIHMLMDRKIVETHAQN 153
 QY 304 ASTQEGELASTQSEELTSLQKHWLSDRTYQOYVYQGTFEDSTRKKADSMPKVSATLS 363
 DB 154 VLIEEGKLASTYSNLNTQOQWSESTFTCKVTSQGENYVAHTRRCSDDEPRGVITYLI 213
 QY 364 RSPFDLFRKSPRTTCLVLDLAPSKGVNLTWASRASKPVNHSTRKEKORNGTLVTS 423
 DB 214 PPSPLDLYENKTPKLTCLVLDL-ESEENITVTWREKKSIGSASORSTKHNMTTITS 272
 QY 424 TLPGVTRDWIEGETYQCRVTHPLPALMSTTSTGPRAPDEVYAFATPEMPSRDKRT 483
 DB 273 ILPVDKDWIEGEGYQCRVTHPLPALMSTTSTGPRAPDEVYAFATPEMPSRDKRT 331
 QY 484 LACTIOMFMPDISVOWLHNEVQLPDAHSTTOPKTKTSGS--FVFSRLVTAEMWPK 541
 DB 332 LTCLIONFPPDISVOWLHNEVQLPDAHSTTOPKTKTSGS--FVFSRLVTAEMWPK 541
 QY 542 DEFICRAVHEAASPSQTVQRAVSVPNG 568
 DB 392 KQTCRVTHALREPRKLERITKSLG 418

RESULT 8
 GC2_CAVPO
 ID GC2_CAVPO STANDARD: PRT: 329 AA.
 AC P01862:
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma-2 chain C region.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE OF 1-3.
 RA Trischmann T.M.;
 RT Submitted (Apr-1975) to the PIR data bank.
 RN [2]
 RP SEQUENCE OF 4-68.
 RX MEDLINE=71058471; PubMed=5538606;
 RA Birtheim B.K., Hussain Q.Z., Gebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
 RT half-cystine joining heavy and light chains.";
 RL Biochemistry 10:18-25(1971).
 RN [3]
 RP SEQUENCE OF 69-133 AND 312-329.
 RX MEDLINE=71058486; PubMed=5538616;
 RA Turner K.J., Gebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
 RT and hinge region cyanogen bromide fragments.";
 RL Biochemistry 10:9-17(1971).
 RN [4]
 RP SEQUENCE OF 134-226.
 RX MEDLINE=75036072; PubMed=4429665;
 RA Tracey D.E., Gebra J.J.;
 RT "Primary structure of the CH2 homology region from guinea pig IgG2

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RT antibodies."
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies."
RL Biochemistry 13:4804-4811(1974).
RN [6]
RX DISULFIDE BONDS.
RP MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamu M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR: A02151; G2GP.
DR HSSP: P01842; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00410; Ig-like; 1.
DR SMART: SM00407; Igcl; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KM Immunoglobulin domain; Immunoglobulin C region; glycoprotein.
FT NON_TER 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 28.0%; Score 858; DB 1; Length 329;
Best Local Similarity 67.4%; Pred. No. 4,1e-52;
Matches 157; Conservative 28; Mismatches 42; Indels 6; Gaps 2;

QY 1 EPKSCDKHTHTCPPEAPPELLGSPVFLPPPKKDTLMTSRTEVYCVVVDVSHDEPEK 60
DB 101 ZPBRG----TCPRKPPRNLCGSPVFTPRPKDTLMTSLPRVTCVVDVSDDEPEYOF 156
QY 61 NWYDGEVHNKVRPREQYNSYRVVSVLTLHONMNGEKCKVSNKALPAPIEKT 120
DB 157 TWFVDNKPVGNAETKPRVEQYNTFRVSVLPIDHODWLRGKEFKKYNKALPAPIEKT 216
QY 121 ISKAKVQPREQVYTLTPSRDELTKNOVSLTCLVKGFTPSDIAVEMESNGQP--ENNYKT 178
DB 217 ISKTKGAPRMPDYVTLTPSRDELTSKSVYTCCLINFPADIHVEMSNRPVSEKEKYN 276
QY 179 TPPLVDVSGSFLLSKLTVDKSRWMOGVNFCSCVMHEALHNHYOORSLSLSPG 231
DB 277 TPPIEDADGSLFLSKLTVDKSRANDOGIVYTCVMHEALHNHYOORSLSRSPG 329

RESULT 9
EPC_MOUSE STANDARD: PRT: 421 AA.
ID EPC_MOUSE
AC P06336; P01856;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig epsilon chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.

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RX MEDLINE=84236092; PubMed=6329728;
RA Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
RT "The nucleotide sequence of the mouse immunoglobulin epsilon gene:
RT comparison with the human epsilon gene sequence."
RL EMBO J. 1:1117-1123(1982).
RN [2]
RP REVISIONS.
RA Honjo T.;
RL Submitted (APR-1986) to the EMBL/Genbank/DBJ databases.
RX SEQUENCE OF 34-421 FROM N.A.
RP MEDLINE=83117774; PubMed=6818553;
RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
RT "Cloning and nucleotide sequence of mouse immunoglobulin epsilon
RT chain cDNA."
RL Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
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DR EMBL: X01857; CAA25977.1;
DR EMBL: X01857; CAA25978.1;
DR PIR: A02145; EHMS.
DR PIR: A02144; EHMS.
DR HSSP: P01854; 11GE.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00410; Ig-like; 2.
DR SMART: SM00407; Igcl; 2.
DR PROSITE: PS00290; IG_MHC; 3.
KM Immunoglobulin domain; Immunoglobulin C region; glycoprotein.
FT NON_TER 1
FT DOMAIN 1 90 CH1.
FT DOMAIN 91 197 CH2.
FT DOMAIN 198 304 CH3.
FT DOMAIN 305 421 CH4.
FT DISULFID 23 75 BY SIMILARITY.
FT DISULFID 121 180 BY SIMILARITY.
FT DISULFID 226 285 BY SIMILARITY.
FT DISULFID 330 392 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 421 AA; 47320 MW; 8F909E1F30A06B47 CRC64;

Query Match 27.0%; Score 826; DB 1; Length 421;
Best Local Similarity 39.4%; Pred. No. 9e-50;
Matches 176; Conservative 80; Mismatches 149; Indels 42; Gaps 11;

QY 129 REPQVYTLTPSRDELTKNOVSLTCLVKGFTPSDIAVEMESNGQPENNYKTPPLVDVSGS 188
DB 3 RNPGLYPLKPKCKGAS---MTLGLTVDPYFPNPTVWYSSLSL-----MSIVNF 49
QY 189 FFLYSKLVDKSR---W-QQGNVFCSCVMHEALHNHYOORSLSLSPKVEGGSGSGGGS 244
DB 50 PALGSELKVTTSQVTSWGSKAKNFTCHVTHPPSPN--ESRILIVPVNI----- 96
QY 245 GGGSGFTPTVYKLIQSSCDGGGHPPTIOLLCVSGTPTGINTITWL-EDGVMDVDLST 303
DB 97 -----TEPIELHSSCDRNA-FHSITQLCYFLYGHILNDVSVWIMDREITDTLAQT 149

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QY 304 ASTOGEELASTOSELTLQKHLMDRTYQVYOGHTFEDSTKCKADSNPRGVSAYLS 363
Db 150 VLIEEGELASTGCKLNTTEQOMMSESTFCCKVTSQGVLYLAHFRCPDHPRGVTYLI 209
QY 364 RPSPEDFIRKSPITTLVLDLADPSKVTNLTWSBASCKPVNHNSTRKEKORNGTLVTS 423
Db 210 PPSPLDLYQNGAPKLTCLVLDLESEK--NVNTWNOEKKTSVSASQWYTKHHNNMTTTSITS 268
QY 424 TLPGTRDMIGETIYOCVTHPHL.PRALMRSTKTSRPAPEVAFATPEMPSRDKRT 483
Db 269 ILPVAKDMIGETIYQCLVDPHDPKPTVRSITKTPGORSAPAEVYVPEPPE--EESSEDKRT 327
QY 484 LACLIONFMPDISYOWLHNEVOLPDARHSTTOPRKTS--GFEVFSRLVETRAEMDOK 541
Db 328 LTLCLIONFMPDISYOWLHNEVOLPDARHSTTOPRKTS--GFEVFSRLVETRAEMDOK 541
QY 542 DEFICRAVHAASPSQTVQRAVSVPNG 568
Db 388 KQFTCOVTHEALOKPRKLEKTISTSLG 414

RESULT 10

QY 10 GCB_RAT STANDARD: PRT: 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR: P50018; P50018.
DR HSSP: P01842; TEAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig: 3.
DR SMART: SM00410; Ig_Like: 1.
DR SMART: SM00407; IgC1: 2.
DR PROSITE: PS00290; Ig_MHC: 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA: 36497 MW: 55F8B64D8D460A6 CRC64;

Query Match 26.6%; Score 813; DB 1; Length 333;
Best Local Similarity 63.6%; Pred. No. 5.2e-49;
Matches 145; Conservative 34; Mismatches 49; Indels 0; Gaps 0;

QY 5 CDKHTCPPCAPPELLGSPVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKRMVY 64
Db 106 CPTCTCHCKCPVPELIGSPVFIFFPKPKDILLISQNAKVTCCVVVDSEEDVDFSWFV 165
QY 65 DGEVHNKTKREBOYNSTYRVSVGLVTLHONMNGKCKYKCKVSKALPAPLEKTSISA 124
Db 166 NNEVHTAOTOPREBOYNSTFRVVSALPIODHDMMSGKEFKCKVNNKALPSPLEKTSIKP 225

QY 125 KVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAMENSGOPENNYKTPPYLD 184
Db 226 KGLVRKPOVYVWGPPTEQLTQVTSLTCLTSGFLPNIDIGVEMTSNGHTEKMYKKEPYMD 285
QY 185 SVGSFELYSKITLVDSKRMQGNVSCSYMHALNHHYQORLSLSGPK 232
Db 286 SDGSFEMYSKLINVERSRWDSRAPVCSVYHGLHNVHKEKISRPPK 333

RESULT 11

QY 11 GC3_MOUSE STANDARD: PRT: 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine Ig3 constant region gene."
RL EMBL J. 3:2041-2046(1984).

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CC EMBL: J00451; NOT_ANNOTATED_CDS.
CC DR PIR: B02156; G3MSC.
DR HSSP: P01857; 1RC1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig: 3.
DR SMART: SM00410; Ig_Like: 1.
DR SMART: SM00407; IgC1: 2.
DR PROSITE: PS00290; Ig_MHC: 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA: 36228 MW: F45827174182BAD6 CRC64;

Query Match 26.6%; Score 812.5; DB 1; Length 329;
Best Local Similarity 64.7%; Pred. No. 5.6e-49;
Matches 145; Conservative 35; Mismatches 41; Indels 3; Gaps 1;

QY 12 PP--CPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKRMVYDGE 68
Db 106 PGSSCPGPNITIGSGSVFIFFPKPKDALLISLTPKVTCCVVVDSEDDPVHVSFWDKNE 165
QY 69 VANNKTKREBOYNSTYRVSVGLVTLHONMNGKCKYKCKVSKALPAPLEKTSISAKYOP 128
Db 166 VHTAMTOPREAOYNSTFRVVSALPIODHDMMSGKEFKCKVNNKALPAPLEKTSIKRGRA 225
QY 129 REPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAMENSGOPENNYKTPPYLDVSGS 188
Db 226 QTPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAMENSGOPENNYKTPPYLDVSGS 188
QY 189 FFLYSKLAVDKSRMOGNGVSCSVMHVALNHHYQORLSLSGPK 232

Db 286 YFLSKLTVDDSDSLQGEIFTCVYHEALHNHHKLNLSRSPGK 329

RESULT 12

GC3M_MOUSE STANDARD: PRT: 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

SEQUENCE FROM N.A.
MEDLINE=85027161; PubMed=6092053;
RA Weis J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
[2]

SEQUENCE OF 328-398 FROM N.A.
MEDLINE=84041483; PubMed=6314258;
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).

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DR EMBL; J00451; AAB59655.1;
DR EMBL; V01526; CAA24767.1; ALT_SEQ.
DR PIR; A02155; G3MSM.
DR HSSP; P01857; IFC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.

DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> O (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).

SEQUENCE 398 AA; 43929 MW; CF7F264B50A1B95 CRC64;
Query Match 26.2%; Score 801.5; DB 1; Length 398;
Best Local Similarity 64.4%; Pred. No. 4, 1e-48;
Matches 143; Conservative 35; Mismatches 41; Indels 3; Gaps 1;

QY 12 P---CPAPLLGSPVFLPPPKRDLMTSRPEVTCVVVDVSHEDPEVKFMYVDGVE 68
DB 106 PPGSSCPGNIIGGSPVFLPPPKRDLMTSLRPFKVCVVVDVSHEDPEVDVHVSFVNDKE 165

QY 69 VHNATKPREQYNSTYRVSVLT/LVHONMNGEKYCKGVSKALPAPIETKISKAYOP 128
DB 166 VHTAWTPREAOYNSTFRVSVLPIHODMNRGKFKCKVNNKALPAPIETISKPKGRA 225
QY 129 REPQYTTLPSPRDELTKNQVSLTCLVKGFYPSDIAVEENSGQPNNKRTTPVLDISGS 188
DB 226 QTPQYTTLPSPRDELTKNQVSLTCLVTNFFSEALISVEVERGELQDYKNTPIIDSDGT 285
QY 189 FFLYSKLTVDKSRMOQNVFSCSVYHEALHNHQQORSLSLP 230
DB 286 YFLYSKLTVDSDSLQGEIFTCVYHEALHNHHKLNLSRSP 327

RESULT 13

GC1_MOUSE STANDARD: PRT: 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

SEQUENCE FROM N.A.
MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
[2]

SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
[3]

SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salsler W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
[4]

SEQUENCE (MYELOMA PROTEIN MOPC 21).
MEDLINE=78242288; PubMed=98524;
RA Adetugbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
murine myeloma gamma1 chain.";
RL J. Biol. Chem. 253:6068-6075(1978).
[5]

DISULFIDE BONDS (MOPC 21).
MEDLINE=73008889; PubMed=5073237;
RA Svastl J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).

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DR EMBL; V00793; CAA24172.1;
DR EMBL; V00793; CAA24173.1;
DR EMBL; V00793; CAA24174.1;

RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Walli R.,
RT "Gene segments encoding transmembrane carboxyl termini of
RT Immunoglobulin gamma chains."
RL Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE-8222190; PubMed-6283537;
RA Yamawaki-Katsoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT Immunoglobulin gamma chains."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC SEGMENT OF MU CHAINS.
CC -----
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CC -----
DR EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR PIR; B02159; G1MSM.
DR HSSP; P01842; 7FAB.
DR MCD; MGI:96446; 19b-4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; 19; 3.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT DISULFID 244 302
FT TRANSMEM 340 357
FT DOMAIN 358 393 POTENTIAL.
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64; CYTOPLASMIC (POTENTIAL).

Query Match 25.68; Score 784.5; DB 1; Length 393;
Best Local Similarity 58.24; Pred. No. 5.9e-47;
Matches 135; Conservative 47; Mismatches 41; Indels 9; Gaps 3;

QY 2 PKSCDTHNCP--CAPELLGSPVFLFPKPKDITMISRTPEVTCVVVDVSHEDPEVK 59
DB 99 PRCG-----CKPCICVPEV--SSVFIFPKPKRDVLTITLTKVTCVVVDISKDPEVQ 151
QY 60 FNNYVDGVEVHANKTKPREQYNSTKRVSVLTITVLHQMNMANGKEYCKYKSKALPAPIEK 119
DB 152 FSNFVDPDVEVHTAQTPREQFNSTFRSVSELPIMHODWLNGKEKCRVNSAAPAPIEK 211
QY 120 TISKAVQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKT 179
DB 212 TISKTRGRPKAPQVYTLIPPKEQMARDKYSLTCTMIDFEFDITVEQMANGQPAENYKNT 271

QY 180 PPVLDSVGSFPLYSKLTIVDKSRWQGNVFSQVMEALHNHYQQRSLSLSPG 231
DB 272 QPIMNTNGSYFVYSKLNWQKSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPG 323

Search completed: July 15, 2003, 06:58:21
Job time : 18.7654 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:54:24 ; Search time 63.9554 Seconds
(without alignments)
1833.165 Million cell updates/sec

Title: US-09-847-208B-7
Perfect score: 3060
Sequence: 1 EPKSCDKHTHPCPCAPPELL.....HEAAPSQTVORAVSNPGK 569

Scoring table: BLASTSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1225 | 40.0 | 471 | 4 | 08TC77 |
| 2 | 1225 | 40.0 | 471 | 4 | 096P08 |
| 3 | 1097 | 35.8 | 473 | 4 | 08TC63 |
| 4 | 877.5 | 28.7 | 337 | 6 | 095M34 |
| 5 | 798.5 | 26.1 | 469 | 11 | 08R3V9 |
| 6 | 795.5 | 26.0 | 463 | 11 | 0991C4 |
| 7 | 791.5 | 25.9 | 437 | 11 | 09R1A4 |
| 8 | 782 | 25.6 | 473 | 11 | 09D8I4 |
| 9 | 772 | 25.2 | 468 | 11 | 0991J1 |
| 10 | 772 | 25.2 | 473 | 11 | 0991J5 |
| 11 | 752.5 | 24.6 | 473 | 11 | 091205 |
| 12 | 752.5 | 24.6 | 474 | 11 | 08R3H6 |
| 13 | 480.5 | 15.7 | 613 | 11 | 08VCX7 |
| 14 | 453.5 | 14.8 | 597 | 4 | 09B0B8 |
| 15 | 448.5 | 14.7 | 597 | 4 | 09B0U0 |
| 16 | 444 | 14.5 | 597 | 4 | 096B89 |

| | | | | | | |
|----|-------|------|-----|----|--------|--------------------|
| 17 | 440.5 | 14.4 | 613 | 4 | 08WUK1 | 08WUK1 homo sapien |
| 18 | 439.5 | 14.4 | 588 | 4 | 08WUX4 | 08WUX4 homo sapien |
| 19 | 439.5 | 14.4 | 618 | 4 | 096AA6 | 096AA6 homo sapien |
| 20 | 438 | 14.3 | 614 | 4 | 096GA6 | 096GA6 homo sapien |
| 21 | 435 | 14.2 | 613 | 4 | 096EY0 | 096EY0 homo sapien |
| 22 | 413 | 13.5 | 375 | 4 | 09BS21 | 09BS21 homo sapien |
| 23 | 399 | 13.0 | 684 | 13 | 090544 | 090544 ginglymosto |
| 24 | 356 | 11.6 | 416 | 4 | 09NPP6 | 09NPP6 homo sapien |
| 25 | 354 | 11.6 | 496 | 4 | 096KX8 | 096KX8 homo sapien |
| 26 | 344.5 | 11.3 | 497 | 4 | 08WY24 | 08WY24 homo sapien |
| 27 | 344 | 11.2 | 494 | 4 | 096K68 | 096K68 homo sapien |
| 28 | 340 | 11.1 | 384 | 4 | 09UP60 | 09UP60 homo sapien |
| 29 | 336.5 | 11.0 | 487 | 11 | 099KA4 | 099KA4 mus musculu |
| 30 | 335 | 10.9 | 482 | 11 | 091X92 | 091X92 mus musculu |
| 31 | 334 | 10.9 | 496 | 4 | 086DK0 | 086DK0 homo sapien |
| 32 | 326.5 | 10.7 | 500 | 4 | 09BRV0 | 09BRV0 homo sapien |
| 33 | 326 | 10.7 | 479 | 11 | 099M22 | 099M22 mus musculu |
| 34 | 324.5 | 10.6 | 481 | 11 | 091WT3 | 091WT3 mus musculu |
| 35 | 322.5 | 10.5 | 481 | 11 | 08VCV5 | 08VCV5 mus musculu |
| 36 | 320 | 10.5 | 488 | 11 | 091WR1 | 091WR1 mus musculu |
| 37 | 319.5 | 10.4 | 484 | 11 | 099LA6 | 099LA6 mus musculu |
| 38 | 317 | 10.4 | 484 | 11 | 08VEA0 | 08VEA0 mus musculu |
| 39 | 313.5 | 10.2 | 489 | 11 | 08VCX4 | 08VCX4 mus musculu |
| 40 | 311 | 10.2 | 486 | 11 | 091Z07 | 091Z07 mus musculu |
| 41 | 309.5 | 10.1 | 481 | 11 | 091WT1 | 091WT1 mus musculu |
| 42 | 305 | 10.0 | 479 | 11 | 091WP5 | 091WP5 mus musculu |
| 43 | 302.5 | 9.9 | 480 | 11 | 091XEL | 091XEL mus musculu |
| 44 | 301.5 | 9.9 | 426 | 11 | 09DCD9 | 09DCD9 mus musculu |
| 45 | 235 | 7.7 | 573 | 4 | 08WU38 | 08WU38 homo sapien |

ALIGNMENTS

RESULT 1
ID 08TC77 PRELIMINARY; PRT; 471 AA.
AC 08TC77;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DR 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC024289; AAH24289.1;
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F74CF588660E CRC64;

| Query Match | Best Local Similarity | Score | 1225; DB 4; | Length | 471; |
|-------------|-----------------------|--|-------------|--------------------|--------|
| Matches | 225; | Conservative | 97.0%; | Pred. No. 1.6e-94; | |
| | | | Mismatches | 3; | Indels |
| | | | | 4; | Gaps |
| | | | | 0; | 0; |
| QY | 1 | EPKSCDKHTHPCPCAPPELLGSPVFLPPPKKDTLMSKTPVYCVVVDVSHDEPKVF | 60 | | |
| DB | 240 | EPKSCDKHTHPCPCAPPELLGSPVFLPPPKKDTLMSKTPVYCVVVDVSHDEPKVF | 299 | | |
| QY | 61 | NMYVDGVVHNWKTFRREOYNSTFRVSVLTVLHQNMMNGKEYCKVSNKALPAPIKKT | 120 | | |
| DB | 300 | NMYVDGVVHNWKTFRREOYNSTFRVSVLTVLHQNMMNGKEYCKVSNKALPAPIKKT | 359 | | |
| QY | 121 | ISKAKVQRPQVYVTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGQPENNYKTP | 180 | | |
| DB | 360 | ISKAKVQRPQVYVTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGQPENNYKTP | 419 | | |
| QY | 181 | PYLDVSGSFLLYKSLTVKSRWOCNVSCSMHMLNHNQORSLSPK | 232 | | |

Db 420 PVLSDSGSFFLYSKLTVDKSRMOQGNVSCSVMHGALHNHYTKSLSPCK 471

RESULT 2

ID 096P08 PRELIMINARY; PRT: 701 AA.

AC 096P08; 01-DEC-2001 (Tremblrel. 19, last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, last sequence update)

DE 01-MAR-2002 (Tremblrel. 20, last annotation update)

DE Factor VII active site mutant immunocoujugate.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21477448; PubMed=11593034;

RA Hu Z., Garen A.;

RT "Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).

DR EMBL; AF272774; AAK58686.1; -.

DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR000742; EGF-2.

DR InterPro: IPR001881; EGF_Ca.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR001254; Ser_protease_Try.

DR InterPro: IPR000294; Vltk_dep_GLA.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00594; gla; 1.

DR Pfam; PF00047; Ig; 2.

DR Pfam; PF00089; trypsin; 1.

DR SMART; SM00181; EGF; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.

DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS00186; EGF_2; UNKNOWN_1.

DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.

DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

DR PROSITE; PS00240; TRYPsin_DOM; 1.

DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.

DR PROSITE; PS00135; TRYPsin_SER; UNKNOWN_1.

KW Hydrolase; Serine protease.

KM

SEQUENCE 701 AA; 77826 MW; 94AC6CB42CC992F CRC64;

Query Match 40.0%; Score 1225; DB 4; Length 701;

Best local Similarity 97.0%; Pred. No. 2.8e-94;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPRSCDTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

DB 470 EPRSCDTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 529

QY 61 NMVVDGEVHNATKPREEOYNSTYRVSVLTVLHOMMNGKEKCKVSKALPAPIEKT 120

DB 530 NMVVDGEVHNATKPREEOYNSTYRVSVLTVLHODMLNGKEKCKVSKALPAPIEKT 569

QY 121 ISRAKVGPREPYVTLPPSDELTKNOVSLTCLVKGFPSPDIADVEMNSQPENNKTPP 180

DB 590 ISRAKVGPREPYVTLPPSDELTKNOVSLTCLVKGFPSPDIADVEMNSQPENNKTPP 649

QY 181 PVLSDSGSFFLYSKLTVDKSRMOQGNVSCSVMHGALHNHYTKSLSPCK 232

DB 650 PVLSDSGSFFLYSKLTVDKSRMOQGNVSCSVMHGALHNHYTKSLSPCK 701

RESULT 3

ID 08TC63 PRELIMINARY; PRT: 473 AA.

AC 08TC63; 01-JUN-2002 (Tremblrel. 21, Created)

DT 01-JUN-2002 (Tremblrel. 21, last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, last annotation update)

DE Hypothetical 52.0 kDa protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY;

RA Strausberg R.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC025985; AAR25985.1; -.

KW Hypothetical protein.

SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 35.8%; Score 1097; DB 4; Length 473;

Best local Similarity 90.5%; Pred. No. 9.3e-84;

Matches 201; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 11 CPSPAPBELLGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKMNVYDGEVH 70

DB 252 CPSPAPBELLGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKMNVYDGEVH 311

QY 71 NVKTKPREEOYNSTYRVSVLTVLHOMMNGKEKCKVSKALPAPIEKTISAKKQPRE 130

DB 312 NAKTKPREEOYNSTYRVSVLTVLHODMLNGKEKCKVSKALPAPIEKTISAKKQPRE 371

QY 131 PÖVYTLPPSRDELTKNOVSLTCLVKGFPSPDIADVEMNSQPENNKTPPVLSDSGSFF 190

DB 372 PÖVYTLPPSRDELTKNOVSLTCLVKGFPSPDIADVEMNSQPENNKTPPVLSDSGSFF 431

QY 191 LYSKLVDKSRMOQGNVSCSVMHGALHNHYTKSLSPCK 232

DB 432 LYSKLVDKSRMOQGNVSCSVMHGALHNHYTKSLSPCK 473

RESULT 4

ID 095M34 PRELIMINARY; PRT: 337 AA.

AC 095M34; 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, last annotation update)

DE Immunoglobulin gamma 1 heavy chain constant region (Fragment).

GN IGHCL.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

NCBI_TaxID=9796;

RN [1]

RP SEQUENCE FROM N.A.

RA Wagner B.;

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

RX SEQUENCE FROM N.A.

RX MEDLINE=98383416; PubMed=9717671;

RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C., Leibold W., Radbruch A.;

RT "Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";

RL Immunobiology 199:105-119(1998).

DR EMBL; AJ300675; CAC44624.1; -.

DR InterPro: IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_2;

FT NON_TER

SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 28.7%; Score 877.5; DB 6; Length 337;

Best local Similarity 67.7%; Pred. No. 1.6e-65;

Matches 157; Conservative 36; Mismatches 36; Indels 3; Gaps 2;

```

QY 3 KSCDKHTCPCCPEELLGGPSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFM
  107 KVCQMS-KCPKCAPPELLGGPSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFM
  165
QY 63 YVDGEVHNKTKPREEOYNSTYRVSVLYLHONMNGKEYCKVSKALPAPIETIS 122
  166 YMDGEVYRTATTRKEEQFNSTYRVSVLYLHODMLSGKEFKCKVNOALPQPIERTIT 225
  123 KAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYSDDIAVEHESNQ--ENNYKTP 180
  226 KTKGRSOPVYVLAHPDELISKVSVTCLVKDFPEPELIEWQNSQPLELTKYSTQ 285
QY 181 PVLDSVGSFFLYSKLTVDKSRMOOGNVSVMHEALHNHYOQKSLSLSPGK 232
  286 AQDSDSGSYFLYKSLTVDKSRMOOGNVSVMHEALHNHYOQKSLSLSPGK 337
  Db
  286 AQDSDSGSYFLYKSLTVDKSRMOOGNVSVMHEALHNHYOQKSLSLSPGK 337

RESULT 5
Q8R3V9 PRELIMINARY: PRT: 469 AA.
AC 08R3V9:
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC024405; AAR24405.1; -.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Query Match 26.1%; Score 798.5; DB 11; Length 469;
Best Local Similarity 59.2%; Pred. No. 1.2e-58;
Matches 138; Conservative 45; Mismatches 41; Indels 9; Gaps 3;

QY 2 PKSCDKHTCPP--CPAPELLGGPSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVK 59
  107 KVCQMS-KCPKCAPPELLGGPSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVK 165
  165
QY 60 FNTYVDGEVHNKTKPREEOYNSTYRVSVLYLHONMNGKEYCKVSKALPAPIETEK 119
  297 FSWFVDVGEVHTAQTTPREEOFNSTFRVSELPIMHODMLSGKEFKCVNSAAPAPIETEK 356
  120 TISAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYSDDIAVEHESNQEPENNYKT 179
  357 TISTKGRKAPQVYTLTPPEKQAKKDVSLTCLMTDFPFEDIYEWQNSQPLELTKYSTQ 416
  Db
  357 TISTKGRKAPQVYTLTPPEKQAKKDVSLTCLMTDFPFEDIYEWQNSQPLELTKYSTQ 416
  180 PVLDSVGSFFLYSKLTVDKSRMOOGNVSVMHEALHNHYOQKSLSLSPGK 232
  417 QPMDTDSGYFLYKSLTVDKSRMOOGNVSVMHEALHNHYOQKSLSLSPGK 469
  QY
  180 PVLDSVGSFFLYSKLTVDKSRMOOGNVSVMHEALHNHYOQKSLSLSPGK 232
  417 QPMDTDSGYFLYKSLTVDKSRMOOGNVSVMHEALHNHYOQKSLSLSPGK 469
  Db
  417 QPMDTDSGYFLYKSLTVDKSRMOOGNVSVMHEALHNHYOQKSLSLSPGK 469

RESULT 6
099LC4 PRELIMINARY: PRT: 463 AA.
AC 099LC4:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC003435; AAR03435.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003600; Ig_1like.
DR InterPro; IPR003606; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igcl; 2.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; Ig_1like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674CB6BC30783 CRC64;

Query Match 26.0%; Score 795.5; DB 11; Length 463;
Best Local Similarity 58.8%; Pred. No. 2e-58;
Matches 137; Conservative 46; Mismatches 41; Indels 9; Gaps 3;

QY 2 PKSCDKHTCPP--CPAPELLGGPSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVK 59
  238 PRDGG---CKPCICTVPEV---SSVFIFPPKPKDVLITLTPKVTGVVDVSHEDPEVK 290
  Db
  238 PRDGG---CKPCICTVPEV---SSVFIFPPKPKDVLITLTPKVTGVVDVSHEDPEVK 290
  QY
  60 FNTYVDGEVHNKTKPREEOYNSTYRVSVLYLHONMNGKEYCKVSKALPAPIETEK 119
  291 FSWFVDVGEVHTAQTTPREEOFNSTFRVSELPIMHODMLSGKEFKCVNSAAPAPIETEK 350
  120 TISAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYSDDIAVEHESNQEPENNYKT 179
  351 TISTKGRKAPQVYTLTPPEKQAKKDVSLTCLMTDFPFEDIYEWQNSQPLELTKYSTQ 410
  Db
  351 TISTKGRKAPQVYTLTPPEKQAKKDVSLTCLMTDFPFEDIYEWQNSQPLELTKYSTQ 410
  QY
  180 PVLDSVGSFFLYSKLTVDKSRMOOGNVSVMHEALHNHYOQKSLSLSPGK 232
  411 QPMDTDSGYFLYKSLTVDKSRMOOGNVSVMHEALHNHYOQKSLSLSPGK 463
  Db
  411 QPMDTDSGYFLYKSLTVDKSRMOOGNVSVMHEALHNHYOQKSLSLSPGK 463

RESULT 7
09RIA4 PRELIMINARY: PRT: 437 AA.
AC 09RIA4:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Gamma1 heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003600; Ig_1like.
DR InterPro; IPR003606; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; Ig; 1.
DR SMART; SM00410; Ig_1like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR NON_TER 1
  FT NON_TER 437
  FT SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

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Query Match 25.9% Score 791.5; DB 11; Length 437;
Best Local Similarity 58.4%; Pred. No. 4.1e-58;
Matches 136; Conservative 47; Mismatches 41; Indels 9; Gaps 3;

QY 2 PRSCDKHTCTCP--CPAPELLGSPSVFLFPKPKDMLISRPPEVTCVYVDVSHEDPEVK 59
DB 212 PRDGC---CPCPCICTYEV---SSVFIFPPKPKADVLTITLPKTCVYVVISKDDPEVQ 264
QY 60 FNMVYDGEVHNKTRPREQYNSTYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEK 119
DB 265 FSMVFYDVEVHTAQTQPREQFNSTFRSVSELPIMHQMNGKEYCKVSNKALPAPIEK 324
QY 120 TISAKVQPREQVYTLTPPSRDELTKNOVSLTCLVKGFPSPDIAYEMESNGQPENNYKTT 179
DB 325 TISTGKPKAPQVYTLTPPREQMAKDVSLTCLMTEDEPDIVYEMQMNQAPAEYKNT 384
QY 180 PPVLDVSGSFYLSKLTVDKSRMOGCVNFSQVMHGLNHNHYOORSLSLSPGK 232
DB 385 QPMDTQSGSYFYVSKLVNOKSNMEAGNTFTCSVLHGLNHNHTKKNLSHSPGK 437

RESULT 8
Q9DBL4 PRELIMINARY; PRT: 473 AA.

ID Q9DBL4
AC Q9DBL4
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE 1810060009Rik protein.
GN IGH-1 OR 1810060009Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Matchanoni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald J., Rodriguez I., Sakamoto N.,
RA Sasaki H., Toyooka K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski A., Yoshida K., Hasegawa Y., Kawanji H., Kohlski S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.",
RL Mature 409:685-690(2001).
DR EMBL: AK007918; BAB25349.1;
DR HSP: P01842; 7FAB.
DR MGD: MGI:96443; Igh-1.
DR InterPro: IPR003599; Ig-1.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig: 4.
DR SMART: SM00409; Ig: 2.
DR SMART: SM00407; Igcl; 3.
DR SMART: SM00406; Igv; 1.
DR SMART: SM00410; Ig_like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.

SEQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
Query Match 25.6% Score 782; DB 11; Length 473;
Best Local Similarity 60.5%; Pred. No. 2.9e-57;
Matches 138; Conservative 39; Mismatches 51; Indels 0; Gaps 0;

QY 5 CDKHTCTCP--CPAPELLGSPSVFLFPKPKDMLISRPPEVTCVYVDVSHEDPEVK 64
DB 246 CPPEKCPKAPDLGGPSVFIFPPKIKDVLMLISPMVTCVYVDVSEDDPQVISMVF 305
QY 65 DGVEYHNKTRPREQYNSTYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISK 124
DB 306 NNVEYHTAQTQTHREDYNTLRVVSALPIQHDMMNGKEYCKVSNKALPAPIEKTISK 365
QY 125 KVQPREQVYTLTPPSRDELTKNOVSLTCLVKGFPSPDIAYEMESNGQPENNYKTT 184
DB 366 RGPVAPQVYTLTPPEAEETKKEFSLTGMITGFLPAEIAVDMTSGNREQYKNTAVLD 425
QY 185 SVGSFYLKLTVDKSRMOGCVNFSQVMHGLNHNHYOORSLSLSPGK 232
DB 426 SDGSYFMYSKLVQKSTWERSLFCASVYHGLNHNHTKKNLSHSPGK 473

RESULT 9
Q99LJ31 PRELIMINARY; PRT: 468 AA.

ID Q99LJ31
AC Q99LJ31
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Similar to RIKEN cDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC003878; AA03878.1;
DR EMBL: BC003878; AA03878.1;
DR HSP: P01842; 7FAB.
DR InterPro: IPR003599; Ig-1.
DR InterPro: IPR003600; Ig-cl.
DR InterPro: IPR003597; Ig_v.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig: 3.
DR SMART: SM00409; Ig: 2.
DR SMART: SM00407; Igcl; 3.
DR SMART: SM00406; Igv; 1.
DR SMART: SM00410; Ig_like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 25.2% Score 772; DB 11; Length 468;
Best Local Similarity 62.9%; Pred. No. 2e-56;
Matches 141; Conservative 31; Mismatches 50; Indels 2; Gaps 1;

QY 11 CPP--CPAPELLGSPSVFLFPKPKDMLISRPPEVTCVYVDVSHEDPEVKFNNYVGVG 68
DB 245 CPPEKCPKAPDLGGPSVFIFPPKIKDVLMLISPMVTCVYVDVSEDDPQVISMVF 304
QY 69 VHNKTRPREQYNSTYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKARVQ 128
DB 305 VLFQAQTQTHREDYNTLRVVSALPIQHDMMNGKEYCKVSNKALPAPIEKTISKPGSV 364
QY 129 REPQVYTLTPPSRDELTKNOVSLTCLVKGFPSPDIAYEMESNGQPENNYKTT 188
DB 365 RAPQVYTLTPPEAEETKKEFSLTGMITGFLPAEIAVDMTSGNREQYKNTAVLD 425
QY 189 FLYLSKLTVDKSRMOGCVNFSQVMHGLNHNHYOORSLSLSPGK 232
DB 425 YFMYSKLVQKSTWERSLFCASVYHGLNHNHTKKNLSHSPGK 468

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RESULT 10
099L25 PRELIMINARY; PRT; 473 AA.
AC 099L25;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to RIKEN cDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AA03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_1like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE989B7986DA155 CRC64;

Query Match 25.2%; Score 772; DB 11; Length 473;
Best Local Similarity 62.9%; Pred. No. 2e-56;
Matches 141; Conservative 31; Mismatches 50; Indels 2; Gaps 1;

OY 11 CPP--CPAPELLGGSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNVVDVSH 68
DB 250 CPCKCPAPNLGGPSVIFPPKIKDYLMISSPVNTCVVDVSHDDVDVQSMFVNVE 309
OY 69 VHNKTKPREDOYNSTYRVSVLTGLVHONMNGKEKCKVSNKALPAPIETISKAKYOP 128
DB 310 VLTAQTQTHREDYNSTLRVSAALPIQHDMMSGKEFKCKVNNKALPAPIERTISKPGSV 369
OY 129 REPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEVESNGQPPNNKTPRPVLDSDGS 188
DB 370 RAPQVYTLPPREEDTKKQVTLTCLVDTFMPEDIVETWNGKTELKNTPEVLDSDGS 429
OY 189 FELSKLTVDKSRMOQGNVFCSVYHREALHNHYOQRSLSLSPGK 232
DB 430 YFMYSKLAVKEKKNNWERNYSYSCSVYHEDLNHHHTTKSRITPK 473

RESULT 11
091205 PRELIMINARY; PRT; 473 AA.
AC 091205;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN A0044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AA010327.1; -.
DR MGI; MGI:2144967; A0044919.
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DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 24.6%; Score 752.5; DB 11; Length 473;
Best Local Similarity 58.6%; Pred. No. 8.7e-55;
Matches 140; Conservative 36; Mismatches 56; Indels 7; Gaps 2;

OY 1 EPKSCDKT-HTCPP-----CPAPELLGGSVFLPPPKPKDTLMISRTPEVTCVVDVSH 53
DB 235 EPSGPISITINCPCKCKCHKCPAPNLBEGSPSVIFPPKIKDYLMISSPVNTCVVDVSE 294
OY 54 EDEPKFNMVYDGVVHNKTKPREDOYNSTYRVSVLTGLVHONMNGKEKCKVSNKAL 113
DB 295 DDPOVQISMFVNNVEVHTAQOTHRREDYNSTLRVSAALPIQHDMMSGKEFKCKVNNKDL 354
OY 114 PAPIETISKAKYQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEVESNGQPE 173
DB 355 PPIERTISKIKGLVRAPOVYTLPPPAQLSRKDVSLTCLVGFNPBGDISVETWSNGHTE 414
OY 174 NNYKTPPVLDSDGSFELYSKLTVDKSRMOQGNVFCSVYHREALHNHYOQRSLSLSPGK 232
DB 415 ENYKDTAVLDSDGSYFIYSKLDIKTSWKEKTDSPSCVNRHGLKNYLLKTKTISRPGK 473
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RESULT 12
08R3H6 PRELIMINARY; PRT; 474 AA.
AC 08R3H6;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 51.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AA025447.1; -.
DR Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 24.6%; Score 752.5; DB 11; Length 474;
Best Local Similarity 58.6%; Pred. No. 8.7e-55;
Matches 140; Conservative 36; Mismatches 56; Indels 7; Gaps 2;

OY 1 EPKSCDKT-HTCPP-----CPAPELLGGSVFLPPPKPKDTLMISRTPEVTCVVDVSH 53
DB 236 EPSGPISITINCPCKCKCHKCPAPNLBEGSPSVIFPPKIKDYLMISSPVNTCVVDVSE 295
OY 54 EDEPKFNMVYDGVVHNKTKPREDOYNSTYRVSVLTGLVHONMNGKEKCKVSNKAL 113
DB 296 DDPOVQISMFVNNVEVHTAQOTHRREDYNSTLRVSAALPIQHDMMSGKEFKCKVNNKDL 355
OY 114 PAPIETISKAKYQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEVESNGQPE 173
DB 356 PPIERTISKIKGLVRAPOVYTLPPPAQLSRKDVSLTCLVGFNPBGDISVETWSNGHTE 415
OY 174 NNYKTPPVLDSDGSFELYSKLTVDKSRMOQGNVFCSVYHREALHNHYOQRSLSLSPGK 232
DB 416 ENYKDTAVLDSDGSYFIYSKLDIKTSWKEKTDSPSCVNRHGLKNYLLKTKTISRPGK 474

RESULT 13
08VCX7 PRELIMINARY; PRT; 613 AA.
ID 08VCX7
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RESULT 15
09BUI0
ID 09BUI0 PRELIMINARY; PRT; 597 AA.
AC 09BUI0;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Hypothetical 65.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH;
RA Strausberg R.;
RL Submitted (FEF-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1;
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 14.7%; Score 448.5; DB 4; Length 597;
Best Local Similarity 24.6%; Pred. No. 4.5e-29;
Matches 143; Conservative 96; Mismatches 267; Indels 75; Gaps 21;

QY 31 KPKDTLMISRPETVCVVVVS-----HEDPEVKFNMYVD---GVEVHNKTKPR 77
DB 32 KPSFTL-----SLTCGVYGSFSGYWSWIRPPGKLEWIGEHNSGSTNYPSLKSR 85
QY 78 EEOYNSTYRVVSVTLVHOMMMNGKEYK-KVSNKALPAPIEK-----TISKAV 126
DB 86 VTISVDTSKKQLSLKSSVNAADAVYYCARVITRASPTDGRGMVWGQITVTVSSG 145
QY 127 QPREPQVYTL-----PPSRDELTKQVSLTCLVKGFTPSDIAVEME-SNGQENNNYKTP 180
DB 146 SASAPTLFPLVSCENSPTS---DTSVAVGCIAODFLPDSITFSMKYKNNSDISSTRGFP 201
QY 181 PYLDVSGSFLYSLKLVWDKSNMOQG--NVFSCSVMHLEAHNHYOQRLSLSPGVKVGCG 238
DB 202 SVLNG-GKIATTSOVLPLPSKDVMOGTDEHYVCKVQHP--NGNKEKNVPL-PVIAE---- 252
QY 239 SGGGSGSGGSGFTPTVKIIQSSCGGSHPEPTIQLCLVSGYPTGITINITLEDQVMD 298
DB 253 -----LPPKVSVPFPRDGFQGNPKRSKLLIQATGFSRQIQVSWLREGQVYG 300
QY 299 VDLSTASTQEGELA-----STQSELTLQKHWLSDRTYTCQVYQGHF-EDSTKCCAD 352
DB 301 SGVTTDOVQAEAKESGPTTYKVTSTLIKESDWLSQSMFTCRVDHRCGLTFQONASSMCP 360
QY 353 SNPRGVSAYLSRPSRPFLEIRKSPITICLVVDLAPSKGTVALTWRSRASKPNVNSTREE 412
DB 361 DQDTAIRFALPSPFASITLKSTKLCLVLDLT-TYDSVTISWTRONGEAVKTHNISE 419
QY 413 KORNGTLVTVSTLPEVGRDWIEGFTYQCRVTHPHLPRALMRSTTKTSGPRA-APEVYAF- 470
DB 420 SHPNATFSVGEASIGCEDDMNSGERFCTVHTHDLPSPLKQTLISRPKGVALLHRDPVILLP 479
QY 471 ATPMPGSRDKRTIACLIONMPEDISYQWILHNEVQLPDARHSTTOR-KTKGSG-FFVF 528
DB 480 PARQOLNLRSATITTCVTGFSPPADVQVOMMOGQPLSPKRYVTSAPMPEDQAPGRYFAH 539

QY 529 SRLVTPRAEWQKDEFICRAVHAASPSQTVORAVSYNPKG 569
DB 540 SILTVSEEWNTGETTYCVVAHRL-PNRVTERTVDKSTCK 579

Search completed: July 15, 2003, 07:01:49
Job time : 64.9554 secs


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FT      /note="Epitope in DE loop"
FT      Region
FT      301..311
FT      /note="Epitope in FG loop"
FT      Region
FT      315..323
FT      /note="Epitope including C3C4 linker"
FT      Region
FT      317..320
FT      /note="Linker between domains C3 and C4"
FT      Domain
FT      321..422
FT      /note="Ige heavy chain C4 domain"
PN      WO200220038-A2.
PD      14-MAR-2002.
XX
XX      06-SEP-2001; 2001WO-DK00579.
XX
XX      06-SEP-2000; 2000DK-0001326.
XX      15-SEP-2000; 2000US-232831P.
XX
XX      (PHAR-) PHARMEXA AS.
XX
XX      Klysner S, Von Hoegen P, Voldborg B, Gautam A;
XX      WPI: 2002-383033/41.
XX
XX      Inducing immune response against autologous immunoglobulin E in an
XX      animal, by effecting simultaneous presentation of cytotoxic T
XX      lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
XX
XX      Examples; Page 101-103; 151pp; English.
XX
XX      This invention relates to a novel method for inducing an immune response
XX      against autologous immunoglobulin E (Ige) in an animal. The method
XX      comprises effecting simultaneous presentation of cytotoxic T lymphocyte
XX      (CTL) epitope and/or B-cell epitope derived from Ige, and T helper cell
XX      epitope (TH epitope) which is foreign to the animal, by antigen
XX      presenting cells (APCs) of the animal's immune system, the epitopes
XX      of the invention may be used as a vaccine against allergic diseases. The
XX      method of the invention is useful for inducing an immune response
XX      against autologous Ige in an animal, which is useful for downregulating
XX      autologous Ige in the animal. This method is useful in the prevention
XX      and treatment of allergic diseases such as anaphylaxis, allergic
XX      rhinitis, asthma and atopic dermatitis. The present sequence represents
XX      the human Ige heavy chain C1-C2-C3-C4 domains used to create the
XX      epitopes of the invention.
XX
XX      Sequence 428 AA:
SQ
Query Match      57.7%; Score 1766; DB 23; Length 428;
Best Local Similarity 78.0%; Pred. No. 9.5e-115;
Matches 347; Conservative 17; Mismatches 57; Indels 24; Gaps 7;
QY      129 REPQVYILPSRDELTKNQVSLT--CLVKGFPYSDIAEVESHNGOPENNYKTP-PVLDS 185
DB      4 QSPVVFPLTRCKKIPSNATSVTLGLATGTFPEPVMTWDT-GSLNQTMTLPAATLTLL 62
QY      186 VGSFVLVSKLVYDSRNQGVNFCQVNHKALNHHY-QQRLSLSPGKVEGGSGSGGGS 244
DB      63 SGHATVLSLTV-SGAWAK-OMFTCRVAHPSSTIDWDNKFFSVC----- 105
QY      245 GGGSGFTPTPYKIIQSSCDGGGHPPTIQLCLVSGTPTGINTITWLEDQGVMDLSTA 304
DB      106 --SNDFTPTPYKIIQSSCDGGGHPPTIQLCLVSGTPTGINTITWLEDQGVMDLSTA 163
QY      305 STTQEGELASTQSELTLSQKHMLSDRYTCQVTVQGHFTFEDSTKCADSNRGVSAVLSR 364
DB      164 STTQEGELASTQSELTLSQKHMLSDRYTCQVTVQGHFTFEDSTKCADSNRGVSAVLSR 223
QY      365 PSPPDLIRKSPPTTCLVNDLAPSKGVNLTWMSASGKPVNHSRKEKQNGTLTYTST 424
DB      224 PSPPDLIRKSPPTTCLVNDLAPSKGVNLTWMSASGKPVNHSRKEKQNGTLTYTST 283

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QY      425 LPVGRDMEIGETTQCRVTHPLPALMRSTTKTSGPPRAAEVYAFATPEWPGSRDKRTL 484
DB      284 LPVGRDMEIGETTQCRVTHPLPALMRSTTKTSGPPRAAEVYAFATPEWPGSRDKRTL 343
QY      485 ACLIQNEPEDIISVQMLNEVQLPARHSTTOPRRTKSGGFVPSRLVETRAEMQRKEF 544
DB      344 ACLIQNEPEDIISVQMLNEVQLPARHSTTOPRRTKSGGFVPSRLVETRAEMQRKEF 403
QY      545 ICRAYHEAASPSQTFQRAVSVNPKR 569
DB      404 ICRAYHEAASPSQTFQRAVSVNPKR 428

RESULT 2
AAM50940
ID      AAM50940 standard; Protein; 428 AA.
XX
XX      AAM50940;
XX
XX      15-MAY-2002 (first entry)
XX
XX      Human Ige epsilon chain constant region.
XX
XX      Ige: immunoglobulin E; antibody; human; allergy; asthma; eczema;
XX      urticaria; anaphylactic shock; allergic rhinitis; conjunctivitis;
XX      anti-anaphylactic; immunosuppressive; antiallergic; antisthmatic;
XX      antiinflammatory; dermatological; vasotropic; ophthalmological;
XX      vaccine; therapy.
XX
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      Domain      1..110
XX      FT      /label= CH1
XX      Domain      313..428
XX      FT      /label= CH4
XX
XX      WO200209751-A2.
XX
XX      07-FEB-2002.
XX
XX      23-JUL-2001; 2001WO-1B01353.
XX
XX      28-JUL-2000; 2000US-221841P.
XX
XX      (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX      (BACH/) BACHMANN M F.
XX      (RENN/) RENNER W A.
XX
XX      Bachmann MF, Renner WA;
XX      WPI: 2002-227076/28.
XX
XX      Composition for treating immunoglobulin (Ig) E-mediated disorder such
XX      as anaphylactic shock, allergic rhinitis and conjunctivitis, comprises
XX      a polypeptide that includes CH1 and/or CH4 domains of Ige molecule
XX      coupled to a carrier.
XX
XX      Claim 41; Page 9; 71pp; English.
XX
XX      The present sequence is that of the human Ige epsilon chain
XX      constant region. The invention is based on the discovery that a
XX      polypeptide that includes the CH1 (i.e. constant domain 1 in the
XX      heavy chain) and/or CH4 domain(s) of an Ige molecule, coupled to a
XX      carrier, can be used to induce in a mammal the production of
XX      antibodies that specifically bind to Ige of the mammal.
XX      Compositions are provided for inducing self-specific anti-Ige
XX      antibodies. These contain carriers foreign to the immunised mammal
XX      coupled to polypeptides containing fragments of the Ige molecule,
XX      especially fragments including the constant CH1 and/or CH4 domain,
XX      but not the CH3 domain. CH1 polypeptides have at least 95% identity
XX      to amino acids 1-110, 105, 5-105 or 5-95 of the present sequence,
XX      while CH4 polypeptides have at least 95% identity to amino acids

```

CC 313-428 313-425, 317-428 or 317-425 of the present sequence. The
CC anti-IGF antibodies reduce or eliminate the pool of free IGF in the
CC mammal's serum. Alternatively, a polynucleotide encoding a fusion
CC protein comprising the carrier and IGF-derived polypeptide is
CC administered. The compositions and polynucleotides are used to
CC inhibit or treat IGF-mediated disorders such as anaphylactic
CC shock, allergic rhinitis or conjunctivitis, an allergic reaction to
CC an allergen such as fur, dust or food, an asthmatic reaction,
CC eczema or urticaria (all claimed).

SQ Sequence 428 AA;

| | | | | |
|-----------------------|------------------|---------------------|------------|-------------|
| Query Match | 57.7% | Score 1766 | DB 23 | Length 428; |
| Best Local Similarity | 76.0% | Pred. No. 9.5e-115; | | |
| Matches 347; | Conservative 17; | Mismatches 115; | Indels 24; | Gaps 7; |

| | | | |
|----|-----|---|-----|
| QY | 129 | REPVOYTLPPERDELTKNOVSLT--CLVKGFEPSDIAEWESNGOPENNYKTTPT--PVLS | 185 |
| Db | 4 | QSPSVFPLTRCKKNIPMSATSVTLGCLLATGTYPEREYVMYTWDT--GSLNGTMTMLPATYTL | 62 |
| QY | 186 | VGSFVFLSKLTVDKSRWQGVNFCSVMHEALHNHY--QORSLSPBKVEGGGGGGGS | 244 |
| Db | 63 | SGHATATISLTLY--SGAMAK--OMETCRVAHTPSSTJMVNDKTSYVC----- | 105 |
| QY | 245 | GGGGSFMPPTKLIIOSSCDGGHPEPTLIOLCLVSGYMPGTINIMLEDOGYMDVLS | 304 |
| Db | 106 | --SKDFTPTPKLIIOSSCDGGGHPEPTLIOLCLVSGYTPGTINIMLEDOGYMDVLS | 163 |
| QY | 305 | STTQEGELASTQSELTLSQKHMLSDRTYTCQVTYOQHTFEDSTKKCADSPNGVASYL | 364 |
| Db | 164 | STTQEGELASTQSELTLSQKHMLSDRTYTCQVTYOQHTFEDSTKKCADSPNGVASYL | 223 |
| QY | 365 | PSPPDLFRKSPPTITCLVVDLAPSKGYVNLWTSRASGRKPVNSTKKEORNGTLVTST | 424 |
| Db | 224 | PSPPDLFRKSPPTITCLVVDLAPSKGYVNLWTSRASGRKPVNSTKKEORNGTLVTST | 283 |
| QY | 425 | LPVTRDIMESETYOCRVTHPLPRALKMRSTKTSGPRAPYVAFATPEMPSRDKRL | 484 |
| Db | 284 | LPVTRDIMESETYOCRVTHPLPRALKMRSTKTSGPRAPYVAFATPEMPSRDKRL | 343 |
| QY | 485 | ACLIONEMPEDISVOMLHNEVOLPDARHSTTQPRKTKSGGFVFSHLEVTRAWEQKDEF | 544 |
| Db | 344 | ACLIONEMPEDISVOMLHNEVOLPDARHSTTQPRKTKSGGFVFSHLEVTRAWEQKDEF | 403 |
| QY | 545 | ICRAVHEAASPQTVQRAVSVNPK | 569 |
| Db | 404 | ICRAVHEAASPQTVQRAVSVNPK | 428 |

RESULT 3
AAM47863

AC AAM47863;

DT 22-FEB-2002 (first entry)

Human Ig-E heavy chain constant region amino acid sequence.

KW Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;
 KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
 KW transgenic plant.

OS Homo sapiens.

PN WO200183529-A2.
XY

PD 08-NOV-2001.
XX

PE 28-APR-2001; 2001WO-US139332;
XY

20-AFN-2000, 200005-200250F-XX
XX

PA (PLAN-) PLANET BIOTECHNOLOGY INC.

PI Larrick JW, Wycoff KL;

DR WPI; 2002-041481/05.
DR N-DCDR; 2PA05378

Immunoadhesin for
XX
XX
DT

PT Immunoadhesin for treating human rhinovirus infection comprises
PT chimeric intercellular adhesion molecule-1, and optionally a J chain
PT and secretory component in association

PS Disclosure; Fig 7; 138pp; English.
xy

CC The invention relates to an immunoadhesin comprising:

rhinovirus receptor protein linked to at least a portion of an immunoglobulin heavy chain: and

(b) optionally a J chain and secretory component associated with the chimeric ICAM-1 molecule. The immunoadhesin has plant-specific

glycosylation and virocyte activity. The immunoadhesin is useful for reducing infection by human rhinovirus (HRV) and hence the initiatic

reduces its infectivity, competing with cell surface ICAM-1 for binding

CC release of viral RNA and formation of empty capsids. Expression of t

CC Immunoadhesin having multiple binding sites have a higher effective

CC Immunoadhesin. Association of secretory component and immunoglobulin

CC environment. Production is significantly less expensive in plants that

CC Since plants are not known to harbor any animal viruses. The present
CC sequence is that of a human immunoglobulin protein sequence. useful

CC the invention.
XX

sequence 428 AA;

| | | | | | | |
|-----------------------|--------|-------|-------|-----------|--------|------|
| query matches | 97.78; | score | 1/00, | db z3, | length | 426; |
| Best local similarity | 78.08; | Pred. | No. | 9.5e-115; | | |

[illegible][illegible]

THE UNIVERSITY OF CHICAGO

[illegible]

205 СТЕПЕНЬ ИСТОСЕТ И СОЖИТ СДБВУТСОУПНУОЧЕПЕДСТККАДНДНДВКВСАУТ

164 STTOECETASTOSEITISOKHWISDBTYTCCOYOGHTEEDSTKKCADSNBRCVSAVI 9

365 PSPFDIETRKSPITTCIYVDIAPSKGTVNI TWSRASGKPVNHSTRKKEEKOBNGTITVTV

Db 224 P S P E D L F I R K S P T I C L V W D L A P S K G T V N L W S R S A S G K P V N H S T R E E K O R M G L F V T S T 283

| | | | |
|----|-----|---|-----|
| Db | 284 | LPVGRDMIEGTTYQCRVYTHPLPRALMNSTTKTSGPRAAPEVYAAATPEWPGSSRCKRTL | 343 |
| QY | 485 | ACLIQNEPEDI SYVOMLHNEVO LDPARHSTTOPRKTKSGGFVEYSLEVTYRAWECKDEF | 544 |
| Db | 344 | ACLIQNEPEDI SYVOMLHNEVO LDPARHSTTOPRKTKSGGFVEYSLEVTYRAWECKDEF | 403 |
| QY | 545 | ICRAVHEAASPQOTVORAVSNPDK | 569 |
| Db | 404 | ICRAVHEAASPQOTVORAVSNPDK | 428 |

RESULT 4

ID AAP40065 standard; Protein; 493 AA.

AAP40065;

12-FEB-1992 (first entry)

Sequence of human immunoglobulin E H-chain.

Antibody; allergy suppressor; immunological.

Homo sapiens.

EPI02634-A.

14-MAR-1984.

03-SEP-1983; 83EP-0108699.

07-SEP-1982; 82JP-0156285.

(TAKE) TAKEDA CHEMICAL IND KK.

Kikuchi M, Kurokawa T, Onda H;

WPI: 1984-070437/12.

N-PSDB; AAN40062.

Polypeptide having activity of human immunoglobulin E - prep.

from host transformed with recombinant DNA

Disclosure: Fig 2; 61pp: English.

DNA encoding Ige H-chain and frags. is claimed (AAN40062).

Transfomant congy. the DNA is also new, esp. Escherichia coli IFO-14284, -5 and -6. The transformant may be grown to produce a

polyptide of immunological or biological activity equivalent to that of the human Ige H chain. AAN40062 or frags. is pref. linked at a

site downstream from a promoter, e.g. rec A promoter (see AAN40064).

Sequence 493 AA;

Query Match 57.5%; Score 1760; DB 5; Length 493;

Best Local Similarity 77.0%; Pred. No. 3e-114; Matches 349; Conservative 14; Mismatches 66; Indels 24; Gaps 7;

QY 120 TISKAKYQREPOVYTLPPSRDELTKNOVSLT--CLVKGFPSPDIAMWESNGOPENNYK 177
 DB 62 TVSSASNTQ--SPSVFPLTRCKKNIPSNATSVTLGCLATGYFPEPYMTWDT--GSLNGTMT 118
 QY 178 TTP-PVLDSVGSFPLYKLYDKSRWQGNVSCSVHMEALHNHYQORSLSLSPKVEGG 236
 DB 119 TLPATFTLTLSGHVATISLTV--SGAMAK-QIFTCRAVHTPSSTVDVNDXTP----- 167
 QY 237 GSGSGGGGGGSGFTPTVKILQSSCDGGHFPPTIOLCLVSGYTGPTITITLWEDGOV 296
 DB 168 -----SVCGRDTPPTVKILQSSCDGGHFPPTIOLCLVSGYTGPTITITLWEDGOV 220
 QY 297 MDVDLASTAQEGELASTOSELTLISQKHWLSDRTYTCOVYQGHTEFEDSTKKCADSNPR 356
 DB 221 MDVDLASTAQEGELASTOSELTLISQKHWLSDRTYTCOVYQGHTEFEDSTKKCADSNPR 280
 QY 357 GVSAYLSRPPFDLFIKRSPTITCLVVDLAPSKGTVNLWMSRASGKPVNSTRKEKORN 416
 DB 281 GVSAYLSRPPFDLFIKRSPTITCLVVDLAPSKGTVNLWMSRASGKPVNSTRKEKORN 340
 QY 417 GTLVFTSLPVGTRDWTIEGEYQCRVTHPHLPRALMSTPTSGPRAPAYATATDEMP 476
 DB 341 GTLVFTSLPVGTRDWTIEGEYQCRVTHPHLPRALMSTPTSGPRAPAYATATDEMP 400

QY 477 GSRDKRTIACLIQNPEDISYQWLHNEVOLDANHSTTOPRKTKGSGFPVFSRLVETRA 536
 DB 401 GSRDKRTIACLIQNPEDISYQWLHNEVOLDANHSTTOPRKTKGSGFPVFSRLVETRA 460
 QY 537 EWEOKDEFICRAVHBAASPSOTVORAVSVNPK 569
 DB 461 EWEOKDEFICRAVHBAASPSOTVORAVSVNPK 493

RESULT 5

ID AAB0287 standard; Protein; 441 AA.

AAB0287;

30-JUL-2002 (first entry)

Human Ige heavy chain C1-C2-C3-C4 domains with MIGIS fragment.

Ige; allergy; human; antiallergic; immunosuppressive; antianaphylactic;

antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; Ige;

vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;

heavy chain C domain; MIGIS.

Homo sapiens.

Synthetic.

OS Synthetic.
 XX Location/Qualifiers
 FH 11..106
 FT /note="Ige heavy chain C1 domain"
 FT 113..208
 FT /label="Ige heavy chain C2 domain"
 FT 205..219
 FT /note="Epitope including C2C3 linker"
 FT 209..216
 FT /note="Linker domain between C2 and C3 region"
 FT 217..317
 FT /note="Ige heavy chain C3 domain"
 FT 244..251
 FT /note="Epitope in BC loop"
 FT 244..251
 FT /note="Epitope in BC loop"
 FT 272..280
 FT /note="Epitope in DE loop"
 FT 301..311
 FT /note="Epitope in FG loop"
 FT 315..323
 FT /note="Epitope including C3C4 linker"
 FT 318..320
 FT /note="Linker between domains C3 and C4"
 FT 321..422
 FT /note="Ige heavy chain C4 domain"
 FT 427..421
 FT /note="MIGIS fragment"
 XX WO200220038-A2.
 XX 14-MAR-2002.
 XX 06-SEP-2001; 2001WO-DK00579.
 XX 06-SEP-2000; 2000DK-0001326.
 XX 15-SEP-2000; 2000US-232831P.
 XX (PHAR-) PHARMAX AS.
 XX Klysner S, Von Hoegen P, Voldborg B, Gautam A;
 XX WPI: 2002-383033/41.
 XX Inducing immune response against autologous immunoglobulin E in an
 XX animal, by effecting simultaneous presentation of cytotoxic T
 XX lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin

PT -
 XX Examples; Page 116-117; 151pp; English.
 PS This invention relates to a novel method for inducing an immune response
 CC against autologous immunoglobulin E (IgE) in an animal. The method
 CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
 CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell
 CC epitope (TH epitope) which is foreign to the animal, by antigen
 CC presenting cells (APCs) of the animal's immune system. The epitopes
 CC of the invention may be used as a vaccine against allergic diseases. The
 CC method of the invention is useful for inducing an immune response
 CC against autologous IgE in an animal, which is useful for downregulating
 CC autologous IgE in the animal. This method is useful in the prevention
 CC and treatment of allergic diseases such as anaphylaxis, allergic
 CC rhinitis, asthma and atopic dermatitis. The present sequence represents
 CC the human IgE heavy chain C1-C2-C3-C4 domains fused to the MGLS
 CC fragment used to create the epitopes of the invention.
 XX
 XX Sequence 441 AA;

Query Match 57.4%; Score 1755; DB 23; Length 441;
 Best Local Similarity 77.9%; Pred. No. 5,7e-114;
 Matches 345; Conservative 17; Mismatches 57; Indels 24; Gaps 7;

OY 129 REPQVYTPPPSDELTKNQVSLT--CLYKGFPSDIAEWESNGCPENNYKTP-PVLD 185
 DB 4 QSPSVFPLTRCKKNIPSNATSVTLGCLATGTFPEPVMYTWDT-GSLNGTMTLPAFTTL 62
 OY 186 VGSFPLYSKLTVDKSRMOQGNFSCVMHEALHNHY--QOSSLISPGKVEGGSGGSGS 244
 DB 63 SGHYATISLITV--SGAMAK-QMFTCRVAH--TSSTWVNKTE----- 105
 OY 245 GGGSEFTPTPKYKILQSSCDGGHFPPTIOLCLVSGYTPGTINITWLEDGQVMDVLS 304
 DB 106 ---SRFTPTPKYKILQSSCDGGHFPPTIOLCLVSGYTPGTINITWLEDGQVMDVLS 163
 OY 305 STTQEGELASTQSELTLQKHWLSDRTYCOVYQYGHFEDSTKKCADSNPRGVSAYLSR 364
 DB 164 STTQEGELASTQSELTLQKHWLSDRTYCOVYQYGHFEDSTKKCADSNPRGVSAYLSR 223
 OY 365 PSPFLTRKSPFTITCLVVDLAPSKGTYNLTWSRASKGVNHSRKEKORNGTLTVST 424
 DB 224 PSPFLTRKSPFTITCLVVDLAPSKGTYNLTWSRASKGVNHSRKEKORNGTLTVST 283
 OY 425 LPVGRDMEIEGETYQCRVTHPHLPALMNSTKTSGPRAAPEVYAFATPEMPSRDKRTL 484
 DB 284 LPVGRDMEIEGETYQCRVTHPHLPALMNSTKTSGPRAAPEVYAFATPEMPSRDKRTL 343
 OY 485 ACLIONFMPEDISVQWLHNEVOLPDARHSTTOPRKTKSGGFVFSRLLEVTRAEMQKDEF 544
 DB 344 ACLIONFMPEDISVQWLHNEVOLPDARHSTTOPRKTKSGGFVFSRLLEVTRAEMQKDEF 403
 OY 545 ICRAYVHEAASPSQTYQRAVSVP 567
 DB 404 ICRAYVHEAASPSQTYQRAVSVP 426

RESULT 6
 AAR42950.
 ID AAR42950 standard; protein; 428 AA.
 XX
 XX AAR42950;
 AC 12-MAY-1994 (first entry)
 DT
 XX
 DE Human IgE heavy chain constant region (residues 120-547).
 XX
 XX Immunoglobulin E; IgE; epsilon heavy chain; IgE receptor binding;
 KW FcR region; allergen; allergic reaction; catalytic antibody;
 KW target sequence.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Region 181..257
 FT /label= "FcR binding region"
 FT /note= "residues 301-376 of IgE H chain, involved
 FT Peptide 105..134
 FT /note= "target peptide I"
 FT Peptide 193..225
 FT /note= "target peptide II"
 PN US5258289-A.
 PD 02-NOV-1993.
 XX
 PD 05-SEP-1990; 90US-0577906.
 XX
 PR 05-SEP-1990; 90US-0577906.
 PR 22-OCT-1991; 91US-0780765.
 XX
 PA (DAVI/) DAVIS C G.
 PI Davis CG, Fabian GR.
 DR WPI, 1993-359735/45.
 XX
 PS Selecting catalytic antibodies which cleave target peptide - used
 PT to block allergic reactions or as preventive treatment
 XX
 XX Example 2; Fig 3; 34pp; English.
 CC Catalytic antibodies which cleave specific target sequences in the
 CC IgE heavy chain constant region are exemplified. Cleavage is
 CC targeted so as to separate the Fab (antigen binding region) from
 CC the Fc region (contg. FcR binding site for attachment to the IgE
 CC receptor on mast cells), thereby destroying receptor binding activity.
 CC The target peptides were selected after consideration of their
 CC primary and secondary structure. The antibodies can be used to block
 CC allergic reactions.
 XX
 SQ Sequence 428 AA;
 Query Match 56.3%; Score 1723; DB 14; Length 428;
 Best Local Similarity 77.7%; Pred. No. 9.3e-112;
 Matches 345; Conservative 14; Mismatches 63; Indels 22; Gaps 7;

OY 129 REPQVYTPPPSDELTKNQVSLT--CLYKGFPSDIAEWESNGCPENNYKTP-PVLD 185
 DB 4 QSPSVFPLTRCKKNIPSNATSVTLGCLATGTFPEPVMYTWDT-GSLNGTMTLPAFTTL 62
 OY 186 VGSFPLYSKLTVDKSRMOQGNFSCVMHEALHNHYQOSSLISPGKVEGGSGGSGS 245
 DB 63 SGHYATISLITV--SGAMAK-QMFTCRVAH-----TSSTWVNKTE-----SV 104
 OY 246 GGGSEFTPTPKYKILQSSCDGGHFPPTIOLCLVSGYTPGTINITWLEDGQVMDVLS 305
 DB 105 CSRDFTPTPKYKILQSSCDGGHFPPTIOLCLVSGYTPGTINITWLEDGQVMDVLS 164
 OY 306 TQEGELASTQSELTLQKHWLSDRTYCOVYQYGHFEDSTKKCADSNPRGVSAYLSR 365
 DB 165 TQEGELASTQSELTLQKHWLSDRTYCOVYQYGHFEDSTKKCADSNPRGVSAYLSR 224
 OY 366 SPFDLFIKSPFTITCLVVDLAPSKGTYNLTWSRASKGVNHSRKEKORNGTLTVSTL 425
 DB 225 SPFDLFIKSPFTITCLVVDLAPSKGTYNLTWSRASKGVNHSRKEKORNGTLTVSTL 284
 OY 426 PVGTRDMEIEGETYQCRVTHPHLPALMNSTKTSGPRAAPEVYAFATPEMPSRDKRTL 485
 DB 286 PVGTRDMEIEGETYQCRVTHPHLPALMNSTKTSGPRAAPEVYAFATPEMPSRDKRTL 344
 OY 486 CLIONFMPEDISVQWLHNEVOLPDARHSTTOPRKTKSGGFVFSRLLEVTRAEMQKDEF 545
 DB 345 CLIONFMPEDISVQWLHNEVOLPDARHSTTOPRKTKSGGFVFSRLLEVTRAEMQKDEF 404

XX Inducing immune response against autologous immunoglobulin E in an
PT animal, by effecting simultaneous presentation of cytotoxic T
PT lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
PT
XX
XX Disclosure; Page 108-110; 151pp; English.
XX
XX This invention relates to a novel method for inducing an immune response
CC against autologous immunoglobulin E (Ige) in an animal. The method
CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
CC (CTL) epitope and/or B-cell epitope derived from Ige, and T helper cell
CC epitope (TH epitope) which is foreign to the animal, by antigen
CC presenting cells (APCs) of the animal's immune system. The epitopes
CC of the invention may be used as a vaccine against allergic diseases. The
CC method of the invention is useful for inducing an immune response
CC against autologous Ige in an animal, which is useful for downregulating
CC autologous Ige in the animal. This method is useful in the prevention
CC and treatment of allergic diseases such as anaphylaxis, allergic
CC rhinitis, asthma and atopic dermatitis. The present sequence represents
CC the human Ige heavy chain C2-C3-C4 domains optimised for expression in a
CC mammalian system, this sequence was used to create the epitopes of the
CC invention.
XX
XX Sequence 323 AA:
SQ
Query Match 55.8%; Score 1707; DB 23; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-111;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 250 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTINITWLEQGVMDVDLSTASTQOE 309
DB 4 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTINITWLEQGVMDVDLSTASTQOE 63
QY 310 GELASTOSELTLSQKHWLSDRTYTCQVYQGHTEFDSRKCADSNPRGVSAVLSRPSFD 369
DB 64 GELASTOSELTLSQKHWLSDRTYTCQVYQGHTEFDSRKCADSNPRGVSAVLSRPSFD 123
QY 370 LFIKSPITITCLVNDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLTVTSLPYGT 429
DB 124 LFIKSPITITCLVNDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLTVTSLPYGT 183
QY 430 RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYATATPEMPSRDKRTIACLIQ 489
DB 184 RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYATATPEMPSRDKRTIACLIQ 243
QY 490 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTKGSGFFFSRLVETVRAEMQKDEFICRAV 549
DB 244 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTKGSGFFFSRLVETVRAEMQKDEFICRAV 303
QY 550 HEASPSQTVORAVSVNPGK 569
DB 304 HEASPSQTVORAVSVNPGK 323
RESULT 9
AAU80286
ID AAU80286 standard; Protein: 323 AA.
XX
XX AAU80286;
XX
XX 30-JUL-2002 (first entry)
XX
XX Human Ige C2-C3-C4 domains for E.Coli expression.
XX
XX Ige; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
KM antilasthmatic; dermatological; antinflammatory; immunoglobulin E; Ige;
KM vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
KV heavy chain C domain.
OS Homo sapiens.
OS Synthetic.
XX

PN W0200220038-A2.
XX
XX 14-MAR-2002.
PD
XX
XX 06-SEP-2001; 2001WO-DK00579.
PF
XX
XX 06-SEP-2000; 2000DK-0001326.
PR
XX 15-SEP-2000; 2000US-232831P.
XX
XX (PHAR-) PHARMEXA AS.
PA
XX
XX Klysner S, Von Hoegen P, Voldborg B, Gautam A;
XX WPI: 2002-383033/41.
DR
XX N-PSDB: ABK51134.
PT
XX
XX Inducing immune response against autologous immunoglobulin E in an
PT animal, by effecting simultaneous presentation of cytotoxic T
PT lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
PT
XX
XX Disclosure; Page 112-113; 151pp; English.
XX
XX This invention relates to a novel method for inducing an immune response
CC against autologous immunoglobulin E (Ige) in an animal. The method
CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
CC (CTL) epitope and/or B-cell epitope derived from Ige, and T helper cell
CC epitope (TH epitope) which is foreign to the animal, by antigen
CC presenting cells (APCs) of the animal's immune system. The epitopes
CC of the invention may be used as a vaccine against allergic diseases. The
CC method of the invention is useful for inducing an immune response
CC against autologous Ige in an animal, which is useful for downregulating
CC autologous Ige in the animal. This method is useful in the prevention
CC and treatment of allergic diseases such as anaphylaxis, allergic
CC rhinitis, asthma and atopic dermatitis. The present sequence represents
CC the human Ige heavy chain C2-C3-C4 domains optimised for expression in
CC an E. Coli system, this sequence was used to create the epitopes of the
CC invention.
XX
XX Sequence 323 AA:
SQ
Query Match 55.8%; Score 1707; DB 23; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-111;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 250 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTINITWLEQGVMDVDLSTASTQOE 309
DB 4 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTINITWLEQGVMDVDLSTASTQOE 63
QY 310 GELASTOSELTLSQKHWLSDRTYTCQVYQGHTEFDSRKCADSNPRGVSAVLSRPSFD 369
DB 64 GELASTOSELTLSQKHWLSDRTYTCQVYQGHTEFDSRKCADSNPRGVSAVLSRPSFD 123
QY 370 LFIKSPITITCLVNDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLTVTSLPYGT 429
DB 124 LFIKSPITITCLVNDLAPSKGTVNLTWASRASKPVNHSRKEKORNGTLTVTSLPYGT 183
QY 430 RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYATATPEMPSRDKRTIACLIQ 489
DB 184 RDWIEGETYQCRVTHPHLPALMRSTTSGPRAPAYATATPEMPSRDKRTIACLIQ 243
QY 490 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTKGSGFFFSRLVETVRAEMQKDEFICRAV 549
DB 244 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTKGSGFFFSRLVETVRAEMQKDEFICRAV 303
QY 550 HEASPSQTVORAVSVNPGK 569
DB 304 HEASPSQTVORAVSVNPGK 323
RESULT 10
AAR83559
ID AAR83559 standard; Protein: 324 AA.

```

XX AAR83559;
AC 06-MAR-1996 (first entry)
DT Fc(epsilon) CH2'-CH4 protein sequence.
DE Fc(epsilon) CH2'-CH4 protein sequence.
XX Fc(epsilon); antibody; human; myeloma; probe; IgE; tryptophan promoter;
KM constant heavy region; E.coli; glycosylation; antigenic; immunogenic;
KW histamine; anti-allergenic; vaccine; immune response.
OS Synthetic.
XX FR2715304-A1.
XX 28-JUL-1995.
PD 26-JAN-1994; 94FR-0000846.
PE 26-JAN-1994; 94FR-0000846.
XX 26-JAN-1994; 94FR-0000846.
PR (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.
PA Hurpin CM, Panero MJM;
XX WPI: 1995-265243/35.
XX N-PSDB; AAT01865.
DR Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain
XX - has epitope(s) not present in native IgE, also derived antibodies
PT for treating or preventing allergies, inflammatory immune disease,
PT etc.
XX Claim 3; Page 32-33; 44pp; French.
XX The amino acid sequence of the Fc(epsilon) CH2'-CH4 fragment covering
XX amino acids 226-547. The DNA sequence was isolated from a human myeloma
CC 266BL CDNA library screened with a probe corresp. to the N-terminus of
CC IgE. The region encoding amino acids 218-547 was cloned into the vector
CC pMT211 under control of the tryptophan promoter. The resultant protein
CC produced contains some non-Fc amino acids. These were removed by
CC replacing their coding sequence with a bicistronic linker. The resultant
CC construct encodes the Fc(epsilon) constant heavy region from amino acids
CC 226-547. When it is expressed in E.coli, the protein produced is a
CC non-glycosylated Fc(epsilon) fragment. Altering the pattern of
CC glycosylation unmasks new antigenic sites thus rendering the Fc fragment
CC immunogenic and able to induce antibodies that recognise native IgE but
CC do not form histamine-releasing complexes. The Fc fragments can be used
CC in anti-allergic vaccines to modulate the intensity of immune responses
CC mediated by IgE.
XX Sequence 324 AA;
SQ
Query Match 55.8%; Score 1707; DB 16; Length 324;
Best Local Similarity 100.0%; Pred. No. 8.5e-111;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 250 FTPTPTVILIOSCDGSGHFPPTIOLCLVSGYPTGTINTIWLDEGQVMDVLDLSTASTQOE 309
DB 5 FTPTPTVILIOSCDGSGHFPPTIOLCLVSGYPTGTINTIWLDEGQVMDVLDLSTASTQOE 64
QY 310 GELASTOSELTLSOKHMLSDRTYCOVYOGHPEFEDSTKRCADSNPBGSAVYSRSPFD 369
DB 65 GELASTOSELTLSOKHMLSDRTYCOVYOGHPEFEDSTKRCADSNPBGSAVYSRSPFD 124
QY 370 LFIKRSPTITCLVVDLAPSKGTNLTWSRASGKRVNSTRKEKORNGTILVTSTLPVGT 429
DB 125 LFIKRSPTITCLVVDLAPSKGTNLTWSRASGKRVNSTRKEKORNGTILVTSTLPVGT 184
QY 430 RDMIEGTYCCRYTHPLPALMRSTTKTSGPRAAPVYAFAPDPWFGSDKRTLACLIQ 489
DB 185 RDMIEGTYCCRYTHPLPALMRSTTKTSGPRAAPVYAFAPDPWFGSDKRTLACLIQ 244

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QY 490 NFMPEDISVQWLNHNEVLPDARHSTTOPRKTKSGGFVFSRLVETRAEMQKDEFICRAV 549
DB 245 NFMPEDISVQWLNHNEVLPDARHSTTOPRKTKSGGFVFSRLVETRAEMQKDEFICRAV 304
QY 550 HEASPQOTVORAVSVNPGK 569
DB 305 HEASPQOTVORAVSVNPGK 324
RESULT 11
AAR75225 ID AAR75225 standard; Protein: 325 AA.
XX AAR75225;
AC 10-NOV-1995 (first entry)
DT Human IgE Fc chain (amino acids 224-547) mutant sequence.
XX IgE Fc fragment; antiallergic.
XX Homo sapiens.
XX Key Location/Qualifiers
FH MISC-difference 149 //label= Asn371
FT //note= "glycosylation site"
FT MISC-difference 172 //label= Asn394
FT //note= "glycosylation site"
FT MISC-difference 1 //label= Val224
FT //note= "any AA or deletion"
FT MISC-difference 2 //label= Cys225
FT //note= "Ala, any other AA, or deletion"
FT MISC-difference 3 //label= Ser226
FT //note= "any AA or deletion"
FT MISC-difference 4 //label= Arg227
FT //note= "any AA or deletion"
FT MISC-difference 5 //label= Asp228
FT //note= "any AA or deletion"
XX WO9514779-A.
XX 01-JUN-1995.
XX 22-NOV-1994; 94WO-GB02561.
XX 22-NOV-1993; 93GB-0024013.
XX (THRE-) 3I RES EXPL LTD.
XX (CLUT ) CELUTECH THERAPEUTICS LTD.
XX Gould HJ, Owens RJ, Sutton BJ, Young RJ;
XX WPI: 1995-206936/27.
XX N-PSDB; AA087474.
XX Mutated glycosylated polypeptide(s) contg. parts of human IgE-Fc
PT useful to study and treat allergy.
XX Disclosure; Page 6; 55pp; English.
XX The sequence represents a mutant sequence of a human IgE-Fc
CC chain (amino acids 224-547) which is of sufficient length to bind
CC Fc-epsilon RI and/or Fc-epsilon FcRI IgE receptor sites on human
CC cells. The protein is useful in the study and treatment of
XX allergy.

```


SQ Sequence 325 AA;
 Query Match 55.8%; Score 1707; DB 16; Length 325;
 Best Local Similarity 100.0%; Pred. No. 8,5e-111;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 FTPTVKILSSCGGGHFPPTIQLCLVSGYTGPTINITWLEGGQVMDVLDSTASTQOE 309
 DB 6 FTPTVKILSSCGGGHFPPTIQLCLVSGYTGPTINITWLEGGQVMDVLDSTASTQOE 65
 QY 310 GELASTOSELTLSOKHMLSDRTYTCQYVYQGHTEFEDSTKRCADSNPRGSAYLSRPSFD 369
 DB 66 GELASTOSELTLSOKHMLSDRTYTCQYVYQGHTEFEDSTKRCADSNPRGSAYLSRPSFD 125
 QY 370 LFIKSPITITCLVVDLAPSKGTNLTWSRASKPVNHSRKEEKORNGTLTSTLPVGT 429
 DB 126 LFIKSPITITCLVVDLAPSKGTNLTWSRASKPVNHSRKEEKORNGTLTSTLPVGT 185
 QY 430 RDWIEGETYQCRVTHPHLPALMRSTTKSGPRAPEYAFATPEWPGSRDKRTLACLIQ 489
 DB 186 RDWIEGETYQCRVTHPHLPALMRSTTKSGPRAPEYAFATPEWPGSRDKRTLACLIQ 245
 QY 490 NFMEEDISVQWLHNEVQLPDARHSTQPRKTKSGFEVFSRLLEYTRAEMQKDEFICRAV 549
 DB 246 NFMEEDISVQWLHNEVQLPDARHSTQPRKTKSGFEVFSRLLEYTRAEMQKDEFICRAV 305
 QY 550 HEASPSQTVORAIVSNPGK 569
 DB 306 HEASPSQTVORAIVSNPGK 325

RESULT 12
 AAR77241
 ID AAR77241 standard; Protein: 325 AA.
 AC AAR77241;
 XX 10-NOV-1995 (first entry)
 DE Human IGE Fc chain (amino acids 224-547) wild-type sequence.
 XX IGE Fc fragment; antiallergic.
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT Misc-difference 149 /label= Asn371
 FT Misc-difference 172 /note= "glycosylation site"
 FT /label= Asn394
 FT /note= "glycosylation site"
 XX
 PN W09514779-A.
 XX
 PD 01-JUN-1995.
 XX
 PF 22-NOV-1994; 94WO-GB02561.
 XX
 PR 22-NOV-1993; 93GB-0024013.
 XX
 PA (THREE-) 31 RES EXPL LTD.
 PA (CLUT) CELTECH THERAPEUTICS LTD.
 XX
 PI Gould HJ, Owens RJ, Sutton BJ, Young RJ;
 DR WPI; 1995-206936/27.
 DR N-PSDB; AA091170.
 XX
 PT Mutated glycosylated polypeptide(s) contg. parts of human IGE-Fc
 XX useful to study and treat allergy.
 PS Disclosure; Page 35-36; 55pp; English.

XX The sequence represents the wild-type sequence of a human IGE-Fc
 CC chain (amino acids 224-547) which is of sufficient length to bind
 CC Fc-epsilon RI and/or Fc-epsilon Fc receptor sites on human
 CC cells. The sequence is preferably mutated (see AAR75225) to
 CC represent a protein encoding a protein where Cys225 is mutated,
 CC optionally together with Val224, Ser226 and Arg227. The protein
 CC is useful in the study and treatment of allergy.
 XX

SQ Sequence 325 AA;
 Query Match 55.8%; Score 1707; DB 16; Length 325;
 Best Local Similarity 100.0%; Pred. No. 8,5e-111;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 FTPTVKILSSCGGGHFPPTIQLCLVSGYTGPTINITWLEGGQVMDVLDSTASTQOE 309
 DB 6 FTPTVKILSSCGGGHFPPTIQLCLVSGYTGPTINITWLEGGQVMDVLDSTASTQOE 65
 QY 310 GELASTOSELTLSOKHMLSDRTYTCQYVYQGHTEFEDSTKRCADSNPRGSAYLSRPSFD 369
 DB 66 GELASTOSELTLSOKHMLSDRTYTCQYVYQGHTEFEDSTKRCADSNPRGSAYLSRPSFD 125
 QY 370 LFIKSPITITCLVVDLAPSKGTNLTWSRASKPVNHSRKEEKORNGTLTSTLPVGT 429
 DB 126 LFIKSPITITCLVVDLAPSKGTNLTWSRASKPVNHSRKEEKORNGTLTSTLPVGT 185
 QY 430 RDWIEGETYQCRVTHPHLPALMRSTTKSGPRAPEYAFATPEWPGSRDKRTLACLIQ 489
 DB 186 RDWIEGETYQCRVTHPHLPALMRSTTKSGPRAPEYAFATPEWPGSRDKRTLACLIQ 245
 QY 490 NFMEEDISVQWLHNEVQLPDARHSTQPRKTKSGFEVFSRLLEYTRAEMQKDEFICRAV 549
 DB 246 NFMEEDISVQWLHNEVQLPDARHSTQPRKTKSGFEVFSRLLEYTRAEMQKDEFICRAV 305
 QY 550 HEASPSQTVORAIVSNPGK 569
 DB 306 HEASPSQTVORAIVSNPGK 325

RESULT 13
 AAB03642
 ID AAB03642 standard; Protein: 331 AA.
 AC AAB03642;
 XX 22-NOV-2000 (first entry)
 DE Human IGE heavy chain constant regions 2, 3 and 4.
 XX Human; immunoglobulin E; IGE; vaccination; infection; allergy;
 XX asthma; eczema; immunogenic peptide.
 OS Homo sapiens.
 XX
 PN W0200025722-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 21-OCT-1999; 99WO-SE01896.
 XX
 PR 02-NOV-1998; 98US-0106652.
 PR 22-SEP-1999; 99US-0401636.
 XX
 PA (RESI-) RESISTENTIA PHARM AB.
 XX
 PI Hellman LF;
 DR WPI; 2000-365342/31.
 DR Immunogenic polypeptides useful for preventing the harmful effects of
 XX immunoglobulin E in mammals -

PS Disclosure: Fig 1; 50pp; English.

CC The present sequence is an immunogenic peptide consisting of the
CC heavy chain constant regions 2, 3 and 4 of the human IGE. It was used to
CC construct a number of immunogenic peptides which consisted of regions of
CC IGE from different mammals, which appear to cause a stronger polyclonal
CC anti-self IGE response than peptides consisting of the same regions from
CC one mammal. Immunogenic peptides, particularly those consisting of
CC different heavy chain constant regions, can be used for vaccination
CC in humans, against bacterial and viral infections and allergies, such
CC as asthma, fur, pollen and food allergies and eczema.

XX Sequence 331 AA;

Query Match 55.8%; Score 1707; DB 21; Length 331;
Best Local Similarity 100.0%; Pred. No. 8.7e-111;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 FTPTVVKILSSCGGHHFPTIQLCLVSGYTGCTINITWLEGGQVNDVLDLSTASTQOE 309
DB 12 FTPTVVKILSSCGGHHFPTIQLCLVSGYTGCTINITWLEGGQVNDVLDLSTASTQOE 71
QY 310 GELASTOSELTLSQKHMLSDRTYTCQVYOGHTFEDSTKCKADSNPRGSAYLSRPSFPD 369
DB 72 GELASTOSELTLSQKHMLSDRTYTCQVYOGHTFEDSTKCKADSNPRGSAYLSRPSFPD 131
QY 370 LPIKSPITITCLVVDLAPSKGTVNLWMSRASKPVNHSRKEKORNGTLVTSTLPVGT 429
DB 132 LPIKSPITITCLVVDLAPSKGTVNLWMSRASKPVNHSRKEKORNGTLVTSTLPVGT 191
QY 430 RDWIEGETYOCRVTHPHLPALMSTTKTSGPRAPEYAFATPEWPGSRDKRTLACLIQ 489
DB 192 RDWIEGETYOCRVTHPHLPALMSTTKTSGPRAPEYAFATPEWPGSRDKRTLACLIQ 251
QY 490 NFMEDISVQWLHNEVOLPDARHSTTOPRKTKSGFVFSRLVETRAEMQKDEFICRAV 549
DB 252 NFMEDISVQWLHNEVOLPDARHSTTOPRKTKSGFVFSRLVETRAEMQKDEFICRAV 311
QY 550 HEAASPSQTVORAVSVNPGK 569
DB 312 HEAASPSQTVORAVSVNPGK 331

RESULT 14

AAP80291 standard; protein: 367 AA.

XX AAP80291;

DT 06-DEC-1990 (first entry)

DE Interleukin-2/IgE Fc fusion protein.

KW Interleukin-2; IGE Fc receptor; fusion protein; asthma; dermatitis.

XX OS synthetic.

FH Key Location/Qualifiers

FT Peptide 1..20

FT Peptide /label=IL-2 leader sequence

FT Peptide 21..31

FT Peptide /label=IL-2 N-terminal

FT Peptide 32..36

FT Peptide /label=linker

FT Peptide 37..367

XX EP269455-A.

XX 01-JUN-1988.

XX 27-NOV-1987; 87EP-0310475.

XX 18-SEP-1987; 87JP-0232295.

PR 28-NOV-1986; 86JP-0281871.

XX (TAKE) TAKEDA CHEMICAL IND KK.

XX Ikeyama S, Nishimura O;

XX WPI: 1988-149211/22.

PR Fused protein for allergy treatment - comprising interleukin-2

PT N-terminal residues, a linker and human immunoglobulin E Fc

PT fragment.

PS Disclosure: ; P; English.

CC This fusion protein has a low toxicity and is useful in therapy

CC for allergy induced by IGE. It can be used in the treatment of

CC allergic dermatosis, atopic dermatitis or bronchial asthma.

XX Sequence 367 AA;

Query Match 55.8%; Score 1707; DB 9; Length 367;
Best Local Similarity 100.0%; Pred. No. 9.9e-111;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 FTPTVVKILSSCGGHHFPTIQLCLVSGYTGCTINITWLEGGQVNDVLDLSTASTQOE 309
DB 48 FTPTVVKILSSCGGHHFPTIQLCLVSGYTGCTINITWLEGGQVNDVLDLSTASTQOE 107
QY 310 GELASTOSELTLSQKHMLSDRTYTCQVYOGHTFEDSTKCKADSNPRGSAYLSRPSFPD 369
DB 108 GELASTOSELTLSQKHMLSDRTYTCQVYOGHTFEDSTKCKADSNPRGSAYLSRPSFPD 167
QY 370 LPIKSPITITCLVVDLAPSKGTVNLWMSRASKPVNHSRKEKORNGTLVTSTLPVGT 429
DB 168 LPIKSPITITCLVVDLAPSKGTVNLWMSRASKPVNHSRKEKORNGTLVTSTLPVGT 227
QY 430 RDWIEGETYOCRVTHPHLPALMSTTKTSGPRAPEYAFATPEWPGSRDKRTLACLIQ 489
DB 228 RDWIEGETYOCRVTHPHLPALMSTTKTSGPRAPEYAFATPEWPGSRDKRTLACLIQ 287
QY 490 NFMEDISVQWLHNEVOLPDARHSTTOPRKTKSGFVFSRLVETRAEMQKDEFICRAV 549
DB 288 NFMEDISVQWLHNEVOLPDARHSTTOPRKTKSGFVFSRLVETRAEMQKDEFICRAV 347
QY 550 HEAASPSQTVORAVSVNPGK 569
DB 348 HEAASPSQTVORAVSVNPGK 367

RESULT 15

AA79994 standard; protein: 325 AA.

XX AA79994;

DT 15-MAY-2000 (first entry)

DE Human immunoglobulin E epsilon heavy chain SEQ ID NO:1.

KW Immunoglobulin E; IGE; epsilon heavy chain; antigenic; antigen;

KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

KW antibody; allergy; allergic disease; immunisation; anti-allergic;

KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Homo sapiens.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13959.

XX 20-JUN-1998; 98US-0100287.

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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:59:40 ; Search time 43.6521 Seconds
(without alignments)
1517.518 Million cell updates/sec

Title: US-09-847-208B-7
Perfect score: 3060
Sequence: 1 EPKSCDKHTPCPCAPPELL.....HEAAPSQTVGRAVSNPGK 569

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|-------------------|--------------------|
| 1 | 3060 | 100.0 | 569 | US-09-847-208-7 | Sequence 7, Appl1 |
| 2 | 1775 | 58.0 | 574 | US-10-047-542-45 | Sequence 45, Appl1 |
| 3 | 1775 | 58.0 | 574 | US-10-214-524-37 | Sequence 37, Appl1 |
| 4 | 1766 | 57.7 | 427 | US-09-847-208-5 | Sequence 5, Appl1 |
| 5 | 1766 | 57.7 | 428 | US-10-047-542-60 | Sequence 60, Appl1 |
| 6 | 1766 | 57.7 | 428 | US-09-949-375A-1 | Sequence 1, Appl1 |
| 7 | 1766 | 57.7 | 428 | US-09-916-230-1 | Sequence 1, Appl1 |
| 8 | 1755 | 57.4 | 592 | US-09-949-375A-7 | Sequence 7, Appl1 |
| 9 | 1729 | 56.5 | 441 | US-10-207-655-334 | Sequence 334, App |
| 10 | 1707 | 55.8 | 320 | US-09-847-208-6 | Sequence 6, Appl1 |
| 11 | 1707 | 55.8 | 323 | US-09-949-375A-2 | Sequence 2, Appl1 |
| 12 | 1707 | 55.8 | 323 | US-09-949-375A-4 | Sequence 4, Appl1 |
| 13 | 1707 | 55.8 | 323 | US-09-949-375A-6 | Sequence 6, Appl1 |
| 14 | 1707 | 55.8 | 331 | US-10-176-664-1 | Sequence 1, Appl1 |
| 15 | 1707 | 55.8 | 331 | US-10-207-655-329 | Sequence 329, App |
| 16 | 1707 | 55.8 | 331 | US-09-401-636-1 | Sequence 1, Appl1 |
| 17 | 1705.5 | 55.7 | 426 | US-10-214-524-26 | Sequence 26, Appl1 |
| 18 | 1696 | 55.4 | 336 | US-09-949-375A-8 | Sequence 8, Appl1 |
| 19 | 1671 | 54.6 | 330 | US-09-949-375A-10 | Sequence 10, Appl1 |

| | | | | | |
|----|--------|------|-----|-------------------|--------------------|
| 20 | 1649 | 53.9 | 347 | US-10-152-190-13 | Sequence 13, Appl1 |
| 21 | 1579 | 51.6 | 347 | US-10-152-190-12 | Sequence 12, Appl1 |
| 22 | 1566.5 | 51.2 | 348 | US-10-152-190-11 | Sequence 11, Appl1 |
| 23 | 1435.5 | 46.9 | 346 | US-10-152-190-10 | Sequence 10, Appl1 |
| 24 | 1364.5 | 44.6 | 346 | US-10-152-190-14 | Sequence 14, Appl1 |
| 25 | 1273.5 | 41.6 | 711 | US-10-071-485-90 | Sequence 90, Appl1 |
| 26 | 1260 | 41.2 | 232 | US-09-847-208-3 | Sequence 3, Appl1 |
| 27 | 1260 | 41.2 | 330 | US-09-847-208-2 | Sequence 2, Appl1 |
| 28 | 1234.5 | 40.3 | 731 | US-09-825-012-46 | Sequence 46, Appl1 |
| 29 | 1234.5 | 40.3 | 741 | US-09-825-012-55 | Sequence 55, Appl1 |
| 30 | 1232 | 40.3 | 660 | US-10-294-055-8 | Sequence 8, Appl1 |
| 31 | 1227 | 40.1 | 543 | US-10-207-655-345 | Sequence 345, App |
| 32 | 1225 | 40.0 | 232 | US-09-996-357-10 | Sequence 10, Appl1 |
| 33 | 1225 | 40.0 | 235 | US-10-207-655-208 | Sequence 208, App |
| 34 | 1225 | 40.0 | 247 | US-09-996-357-13 | Sequence 13, Appl1 |
| 35 | 1225 | 40.0 | 251 | US-10-008-063-18 | Sequence 18, Appl1 |
| 36 | 1225 | 40.0 | 251 | US-10-152-363A-6 | Sequence 6, Appl1 |
| 37 | 1225 | 40.0 | 267 | US-09-996-357-12 | Sequence 12, Appl1 |
| 38 | 1225 | 40.0 | 288 | US-09-822-851B-14 | Sequence 14, Appl1 |
| 39 | 1225 | 40.0 | 288 | US-10-119-637A-14 | Sequence 14, Appl1 |
| 40 | 1225 | 40.0 | 330 | US-10-047-542-20 | Sequence 20, Appl1 |
| 41 | 1225 | 40.0 | 330 | US-09-996-898A-15 | Sequence 15, Appl1 |
| 42 | 1225 | 40.0 | 330 | US-09-892-949-38 | Sequence 38, Appl1 |
| 43 | 1225 | 40.0 | 330 | US-10-269-805-68 | Sequence 68, Appl1 |
| 44 | 1225 | 40.0 | 331 | US-10-341-836-2 | Sequence 2, Appl1 |
| 45 | 1225 | 40.0 | 332 | US-09-990-586-98 | Sequence 98, Appl1 |

ALIGNMENTS

RESULT 1

US-09-847-208-7
Sequence 7, Application US/09847208
Publication No. US20030082190A1
GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
APPLICANT: zhang, ke
APPLICANT: zhu, Daocheng
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 569
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4
OTHER INFORMATION: (19E)
US-09-847-208-7

Query Match 100.0%: Score 3060; DB 9; Length 569;

Best Local Similarity 100.0%: Pred. No. 8.5e-181; Mismatches 0; Indels 0; Gaps 0;

Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTPCPCAPPELLGGPSVFLFPPPKKDTLMSIRPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKHTPCPCAPPELLGGPSVFLFPPPKKDTLMSIRPEVTCVVVDVSHEDPEVKF 60
QY 61 NMVYGVGEVHNKTKPREEQYNSTYRVVSVLTFLHQMNMNGKEYCKSNALPAPIKRT 120
DB 61 NMVYGVGEVHNKTKPREEQYNSTYRVVSVLTFLHQMNMNGKEYCKSNALPAPIKRT 120
QY 121 ISKAVQPREPOVYTLPSRDELTKNQVSLTCLGVGFPSDIAVEMESNGQPENNYKTPP 180
DB 121 ISKAVQPREPOVYTLPSRDELTKNQVSLTCLGVGFPSDIAVEMESNGQPENNYKTPP 180
QY 181 PVLDSVGSFYLTKLVTKSRMVGQVNFSCSYMHDLNHNHQQRSLSLSPCKVEGSGSG 240
DB 181 PVLDSVGSFYLTKLVTKSRMVGQVNFSCSYMHDLNHNHQQRSLSLSPCKVEGSGSG 240

Db 181 PVLDSVGSFLLXSKLTVDKSRMOGNVFCVSMHMLNHNHVOQRSLSPGKVEGGSSG 240
Qy 241 GGGSGGGGFTPPYVKIIQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEGGVMD 300
Db 241 GGGSGGGGFTPPYVKIIQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEGGVMD 300
Qy 301 LSTASTOEGELASTOSELTSOKHMLSORTTCOVYOGHFEEDSTKCADSNRGSA 360
Db 301 LSTASTOEGELASTOSELTSOKHMLSORTTCOVYOGHFEEDSTKCADSNRGSA 360
Qy 361 YLSRSPDFLIRKSPITITCLVVDLAPSKGTYNLWMSASGKPVNHSRKEKQNGILY 420
Db 361 YLSRSPDFLIRKSPITITCLVVDLAPSKGTYNLWMSASGKPVNHSRKEKQNGILY 420
Qy 421 VTSLPVTGTRMIEGETYQCRVTHPHLPALMRSTTKSGPRADEVYAFATPEWGSRD 480
Db 421 VTSLPVTGTRMIEGETYQCRVTHPHLPALMRSTTKSGPRADEVYAFATPEWGSRD 480
Qy 481 KRTIACLIOMFPEDISVQWMLHNEVQLPDARHSTTOPRKTGSGFFVSRLEVTAEWEO 540
Db 481 KRTIACLIOMFPEDISVQWMLHNEVQLPDARHSTTOPRKTGSGFFVSRLEVTAEWEO 540
Qy 541 KDEFICRAVHEAASPSQTVORAVSNPGK 569
Db 541 KDEFICRAVHEAASPSQTVORAVSNPGK 569

RESULT 2

US-10-047-542-45
: Sequence 45, Application US/10047542
: Patent No. US20020168367A1
: GENERAL INFORMATION:
: APPLICANT: LARRICK, JAMES W.
: APPLICANT: WICOF, KEITH L.
: TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
: FILE REFERENCE: 030905.0004.C1P1
: CURRENT APPLICATION NUMBER: US/10/047,542
: PRIOR FILING DATE: 2001-10-26
: PRIOR APPLICATION NUMBER: PCT/US01/13932
: PRIOR FILING DATE: 2001-04-28
: PRIOR APPLICATION NUMBER: 60/200,298
: NUMBER OF SEQ ID NOS: 101
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 45
: LENGTH: 574
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-047-542-45

Query Match 58.0%; Score 1775; DB 9; Length 574;
Best Local Similarity 77.3%; Pred. No. 1.1e-101;
Matches 351; Conservative 17; Mismatches 60; Indels 26; Gaps 8;

Qy 120 TISAKAVOPREPOYYTLPPSRDELTKNOVSLT--CLVKGYPDSIAVEMESNGPENNYK 177
Db 143 TVSSASTQ--SPSYFPLTRCCKNIPSNATSVTLGLATGTFPEPVMTWTD--GSLNGTMM 199
Qy 178 TTP-PVLDSVGSFELYKLTVDKSRMOGNVFCVSMHMLNHNH--QORSLSLPGKVEG 235
Db 200 TLPATITLISGHVATISLTV-SGAMAK-QMFTCRVAHFTPSSTDMVNKTFEVC----- 251
Qy 236 GGGSGGGGSGGSGFTPPYVKIIQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEGGQ 295
Db 252 -----SRDFTPPTVYKIIQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEGGQ 300
Qy 296 VMDVLDSTASTOEGELASTOSELTSOKHMLSORTTCOVYOGHFEEDSTKCADSNP 355
Db 301 VMDVLDSTASTOEGELASTOSELTSOKHMLSORTTCOVYOGHFEEDSTKCADSNP 360
Qy 356 RGVSAVLSRSPDFLIRKSPITITCLVVDLAPSKGTYNLWMSRASKPVNHSRKEEOR 415
Db 356 RGVSAVLSRSPDFLIRKSPITITCLVVDLAPSKGTYNLWMSRASKPVNHSRKEEOR 415

Db 361 RGVSAVLSRSPDFLIRKSPITITCLVVDLAPSKGTYNLWMSRASKPVNHSRKEEOR 420
Qy 416 NGTLVTSTLPVGRDMIEGETYQCRVTHPHLPALMRSTTKSGPRADEVYAFATPEW 475
Db 421 NGTLVTSTLPVGRDMIEGETYQCRVTHPHLPALMRSTTKSGPRADEVYAFATPEW 480
Qy 476 PGSDKRTIACLIOMFPEDISVQWMLHNEVQLPDARHSTTOPRKTGSGFFVSRLEVT 535
Db 481 PGSDKRTIACLIOMFPEDISVQWMLHNEVQLPDARHSTTOPRKTGSGFFVSRLEVT 540
Qy 536 AEMEOKDEFICRAVHEAASPSQTVORAVSNPGK 569
Db 541 AEMEOKDEFICRAVHEAASPSQTVORAVSNPGK 574

RESULT 3

US-10-214-524-37
: Sequence 37, Application US/10214524
: Publication No. US20030073142A1
: GENERAL INFORMATION:
: APPLICANT: Chen, Swei-Shen Alex
: APPLICANT: Yang, Yong-Min
: APPLICANT: Barankiewicz, Theresa J.
: APPLICANT: Chen, Zhong
: TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
: FILE REFERENCE: 16-00101.P.1.1
: CURRENT APPLICATION NUMBER: US/10/214,524
: PRIOR FILING DATE: 2002-08-08
: PRIOR APPLICATION NUMBER: 60/312,120
: PRIOR FILING DATE: 2001-08-13
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 37
: LENGTH: 574
: TYPE: PRT
: ORGANISM: Human (Homo sapiens)
US-10-214-524-37

Query Match 58.0%; Score 1775; DB 9; Length 574;
Best Local Similarity 77.3%; Pred. No. 1.1e-101;
Matches 351; Conservative 17; Mismatches 60; Indels 26; Gaps 8;

Qy 120 TISAKAVOPREPOYYTLPPSRDELTKNOVSLT--CLVKGYPDSIAVEMESNGPENNYK 177
Db 143 TVSSASTQ--SPSYFPLTRCCKNIPSNATSVTLGLATGTFPEPVMTWTD--GSLNGTMM 199
Qy 178 TTP-PVLDSVGSFELYKLTVDKSRMOGNVFCVSMHMLNHNH--QORSLSLPGKVEG 235
Db 200 TLPATITLISGHVATISLTV-SGAMAK-QMFTCRVAHFTPSSTDMVNKTFEVC----- 251
Qy 236 GGGSGGGGSGGSGFTPPYVKIIQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEGGQ 295
Db 252 -----SRDFTPPTVYKIIQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEGGQ 300
Qy 296 VMDVLDSTASTOEGELASTOSELTSOKHMLSORTTCOVYOGHFEEDSTKCADSNP 355
Db 301 VMDVLDSTASTOEGELASTOSELTSOKHMLSORTTCOVYOGHFEEDSTKCADSNP 360
Qy 356 RGVSAVLSRSPDFLIRKSPITITCLVVDLAPSKGTYNLWMSRASKPVNHSRKEEOR 415
Db 361 RGVSAVLSRSPDFLIRKSPITITCLVVDLAPSKGTYNLWMSRASKPVNHSRKEEOR 420
Qy 416 NGTLVTSTLPVGRDMIEGETYQCRVTHPHLPALMRSTTKSGPRADEVYAFATPEW 475
Db 421 NGTLVTSTLPVGRDMIEGETYQCRVTHPHLPALMRSTTKSGPRADEVYAFATPEW 480
Qy 476 PGSDKRTIACLIOMFPEDISVQWMLHNEVQLPDARHSTTOPRKTGSGFFVSRLEVT 535
Db 481 PGSDKRTIACLIOMFPEDISVQWMLHNEVQLPDARHSTTOPRKTGSGFFVSRLEVT 540
Qy 536 AEMEOKDEFICRAVHEAASPSQTVORAVSNPGK 569
Db 541 AEMEOKDEFICRAVHEAASPSQTVORAVSNPGK 574

| | | | | |
|----------------------|-----------------|--------------------|-----------|------------|
| Query Match | 57.7% | Score 1766 | DB 9 | Length 427 |
| Best Local Similarly | 78.0% | Pred. No. 2.8e-101 | | |
| Matches 347 | Conservative 17 | Mismatches 57 | Indels 24 | Gaps 7 |

RESULT 5
US-10-047-542-60
; Sequence 60, Application US/10047542
; Patent No. US20020168367A1

| QY | DB | Sequence | Score | DB % | Length | Matches | Conservative | Mismatches | Indels | Gaps |
|----|----|--|-------|------|--------|---------|--------------|------------|--------|------|
| QY | DB | 129 REPQVYLLPPSRDELTKNQVSLT-CLVKGFYPSDIAEVESNGCPENNYKTT-PVLDS | 57.7% | 1766 | 428 | 78.0% | 17 | 57 | 24 | 7 |
| QY | DB | 4 QSPVFPLTRCKKNIPSNATSVTLQCLATGYFPEPVMTWDP-GSLNGTMTLPTTLTL | 78.0% | 101 | 101 | 100% | 0 | 0 | 0 | 0 |
| QY | DB | 186 VGSEFFLSKLTVDKSRMQGNVFCSCVMEALHNHY-QORSLSPGKVEGGGSGGGGS | 78.0% | 101 | 101 | 100% | 0 | 0 | 0 | 0 |
| QY | DB | 63 SGHATISLTLV-SGAAAK-QMFCIRVAHFTSSIDWVNKRTSVC----- | 78.0% | 101 | 101 | 100% | 0 | 0 | 0 | 0 |
| QY | DB | 245 GGGGSETPPYTKLIQSSCDGGGHPPTIQLCLVSGVYPGTINITWLEDGQYMDVLSLA | 78.0% | 101 | 101 | 100% | 0 | 0 | 0 | 0 |
| QY | DB | 106 --SRDFPPPYTKLIQSSCDGGGHPPTIQLCLVSGVYPGTINITWLEDGQYMDVLSLA | 78.0% | 101 | 101 | 100% | 0 | 0 | 0 | 0 |
| QY | DB | 305 STQEGELASQSELTLSQKHWLSORTYTCQVYCGHFEEDSTKCADSNPGVSAYLSR | 78.0% | 101 | 101 | 100% | 0 | 0 | 0 | 0 |
| QY | DB | 164 STQEGELASQSELTLSQKHWLSORTYTCQVYCGHFEEDSTKCADSNPGVSAYLSR | 78.0% | 101 | 101 | 100% | 0 | 0 | 0 | 0 |
| QY | DB | 365 PSPEDLFRKSPITICLVVDLAPSKGTYNLTWSRASGRPVNSTRKEEKORNGTLTVST | 78.0% | 101 | 101 | 100% | 0 | 0 | 0 | 0 |
| QY | DB | 224 PSPEDLFRKSPITICLVVDLAPSKGTYNLTWSRASGRPVNSTRKEEKORNGTLTVST | 78.0% | 101 | 101 | 100% | 0 | 0 | 0 | 0 |
| QY | DB | 425 LPVGRDMEIEGETYQCRVTHHPLPALMRSTTKTSGPRAAPVYAFATPEWGSRDRTL | 78.0% | 101 | 101 | 100% | 0 | 0 | 0 | 0 |
| QY | DB | 284 LPVGRDMEIEGETYQCRVTHHPLPALMRSTTKTSGPRAAPVYAFATPEWGSRDRTL | 78.0% | 101 | 101 | 100% | 0 | 0 | 0 | 0 |
| QY | DB | 485 ACLIQNFMPEIDISVQMLNEVQLPDARHSTQPRKTKSGGFVFSRLLEYTRAEMQKDEF | 78.0% | 101 | 101 | 100% | 0 | 0 | 0 | 0 |
| QY | DB | 344 ACLIQNFMPEIDISVQMLNEVQLPDARHSTQPRKTKSGGFVFSRLLEYTRAEMQKDEF | 78.0% | 101 | 101 | 100% | 0 | 0 | 0 | 0 |
| QY | DB | 545 ICRAVHEAASPSQTVQRAVSNPGK 569 | 78.0% | 101 | 101 | 100% | 0 | 0 | 0 | 0 |
| QY | DB | 404 ICRAVHEAASPSQTVQRAVSNPGK 428 | 78.0% | 101 | 101 | 100% | 0 | 0 | 0 | 0 |


```

: LENGTH: 441
: TYPE: PRT
: ORGANISM: homo sapiens
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (11)..(106)
: OTHER INFORMATION: Ige heavy chain C1 domain
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (113)..(208)
: OTHER INFORMATION: Ige heavy chain C2 domain
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (217)..(317)
: OTHER INFORMATION: Ige heavy chain C3 domain
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (321)..(422)
: OTHER INFORMATION: Ige heavy chain C4 domain
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (427)..(441)
: OTHER INFORMATION: MISC fragment
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (209)..(216)
: OTHER INFORMATION: Linker between domains C2 and C3
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (318)..(320)
: OTHER INFORMATION: Linker between domains C3 and C4
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (205)..(219)
: OTHER INFORMATION: Epitope including C2C3 linker
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (315)..(323)
: OTHER INFORMATION: Epitope including C3C4 linker
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (244)..(251)
: OTHER INFORMATION: Epitope in BC loop
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (272)..(280)
: OTHER INFORMATION: Epitope in DE loop
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (301)..(311)
: OTHER INFORMATION: Epitope in FG loop
US-09-949-375A-7

Query Match          57.4%; Score 1755; DB 9; Length 441;
Best Local Similarity 77.9%; Pred. No. 1.4e-100;
Matches 345; Conservative 17; Mismatches 57; Indels 24; Gaps 7;

OY 129 REPQYTLPPSRDELTKNOVSLT--CLVKGFPYSDIAVEMESNGQPENNYKTP- PVLDS 185
DB 4 QSPSFFPLTRCKKNIPSNATVTLGLATGYFPEVVMWTDT- GSLNGTMTLTPATTLTL 62
OY 186 VGSFELYSLTVDSRMOQGNVFSQVMEALHNHY--QORSLSLSPKVEGGSGSGGS 244
DB 63 SGHATISLTLV-SGAMAK-QMFTCRVAHPTPSSTDWVNKTFYSV- 105
OY 245 GGGSGFTPPYKIIQSSCDGGGHPPTIQLCLVSGYTPGTINTWLEDGOVMDVLSLA 304
DB 106 --SRFTPPYKIIQSSCDGGGHPPTIQLCLVSGYTPGTINTWLEDGOVMDVLSLA 163
OY 305 STTQGGELASTOSSELTLSQKHWLSRRTTCOVYTOGHFFEDSTKCKADSNRGVSAVYSR 364
DB 164 STTQGGELASTOSSELTLSQKHWLSRRTTCOVYTOGHFFEDSTKCKADSNRGVSAVYSR 223
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OY 365 PSPDFLRKSPITTCVLVDLAPSKGTVNLWTSRASKGPNVHSTRKEKORNGTLVTST 424
DB 224 PSPDFLRKSPITTCVLVDLAPSKGTVNLWTSRASKGPNVHSTRKEKORNGTLVTST 263
OY 425 LPVGTDMIGETVQCVTHPHLPRALMRSTTKTSGPRAAPVYAFATPEMPSGRDKRTL 484
DB 284 LPVGTDMIGETVQCVTHPHLPRALMRSTTKTSGPRAAPVYAFATPEMPSGRDKRTL 343
OY 485 ACLIQNMPEDISVQWLHNEVQLPDARHSTTORPKTGSGFPVSRLEVTRAEWDKDER 544
DB 344 ACLIQNMPEDISVQWLHNEVQLPDARHSTTORPKTGSGFPVSRLEVTRAEWDKDER 403
OY 545 ICRVHEAASPTQTVQRAVSYP 567
DB 404 ICRVHEAASPTQTVQRAVSYP 426

RESULT 9
US-10-207-655-334
: Sequence 334, Application US/10207655
: Publication No. US20030118592A1
: GENERAL INFORMATION:
: APPLICANT: Ledbetter, Jeffrey A.
: TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
: FILE REFERENCE: 390069.401C1
: CURRENT APPLICATION NUMBER: US/10/207, 655
: CURRENT FILING DATE: 2002-07-25
: NUMBER OF SEQ ID NOS: 426
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 334
: LENGTH: 592
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: fusion polypeptide
US-10-207-655-334

Query Match          56.5%; Score 1729; DB 9; Length 592;
Best Local Similarity 60.9%; Pred. No. 7.7e-99;
Matches 358; Conservative 15; Mismatches 51; Indels 164; Gaps 9;

OY 126 VQPREQYTLPPSRDELTKNOVSLTCLVKG-----FY---PSDIAVEMESNGQPENNY 176
DB 25 VLSSPALSLASPG-----EKVTMTCRASSVSVMHYQOKPSSSPKPMY--APSNLA 76
OY 177 KTPPPVLDSVGSFPLYSKLTVDKSRMOQGNVFSQVMEALHNHYQORSL--SLSPG-- 231
DB 77 SGVPAFSGSGSGSTSYS-LTISRVEADEAATYYC-----QQWSENPPTFGAGTK 124
OY 232 -KVEGGSGSGSGSGSGSGS----- 249
DB 125 LELKGGGSGSGSGSGSGSGSQAAYLQOSGAELVPRGASVKMSCKASGYTFTSYNMHWKOT 184
OY 250 ----- 249
DB 185 PROGLEWIGATYPNGDSTYNQKFKKATLVDSKSRATVQMSLTSSEDSAVYFCARVY 244
OY 250 ----- 249
DB 250 ----- 249
OY 250 ----- 249
DB 245 YYSNMYFDVWAGTGTVTYVSDHVCSDRFPPTVKIIQSSCDGGGHPPTIQLCLVSGY 304
OY 282 TPGTINTWLEDGOVMDVLSASTQGGELASTOSSELTLSQKHWLSRRTTCOVYTOGH 341
DB 305 TPGTINTWLEDGOVMDVLSASTQGGELASTOSSELTLSQKHWLSRRTTCOVYTOGH 364
OY 342 TFEEDSTKCKADSNRGVSAVYSRSPFDLFRKSPITTCVLVDLAPSKGTVNLWTSRASK 401
DB 365 TFEEDSTKCKADSNRGVSAVYSRSPFDLFRKSPITTCVLVDLAPSKGTVNLWTSRASK 424
OY 402 KPVNHSTRKEKORNGTLVTSTLPVGTDMIGETVQCVTHPHLPRALMRSTTKTSGP 461
DB 425 KPVNHSTRKEKORNGTLVTSTLPVGTDMIGETVQCVTHPHLPRALMRSTTKTSGP 484
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OY 462 RAAPVYAFATPEWPGSRDKRTLACLIONFMPEDISVOMLHNEVOLDPARHSTTOPRRTK 521
:
:
:
DB 485 RAAPVYAFATPEWPGSRDKRTLACLIONFMPEDISVOMLHNEVOLDPARHSTTOPRRTK 544
:
:
:
OY 522 GSGFFVFSRLLEVTRAEMQKDEFICRAVHEAASPSQTVORAVSNPGK 569
:
:
:
DB 545 GSGFFVFSRLLEVTRAEMQKDEFICRAVHEAASPSQTVORAVSNPGK 592
:
:
:
RESULT 10
US-09-847-208-6
: Sequence 6, Application US/09847208
: Publication No. US20030082190A1
: GENERAL INFORMATION:
: APPLICANT: Saxon, Andrew
: APPLICANT: Zhang, Ke
: APPLICANT: Zhu, Daocheng
: TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
: TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
: FILE REFERENCE: US67,002A
: CURRENT APPLICATION NUMBER: US/09/847,208
: CURRENT FILING DATE: 2001-05-01
: NUMBER OF SEQ ID NOS: 177
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 320
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-847-208-6

Query Match 55.8%; Score 1707; DB 9; Length 320;
Best Local Similarity 100.0%; Pred. No. 8.8e-96;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 250 FTPTVKILQSSCGGHHFPTIOLCLVSGYTPGTINITWLEGGVMDVLDLSTASTOE 309
:
:
:
DB 1 FTPTVKILQSSCGGHHFPTIOLCLVSGYTPGTINITWLEGGVMDVLDLSTASTOE 60
:
:
:
OY 310 GELASTOSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCADSNPBGVSAIYLSRPSFD 369
:
:
:
DB 61 GELASTOSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCADSNPBGVSAIYLSRPSFD 120
:
:
:
OY 370 LFIKSPITICLVVDLAPSKGTVNLTWRSRSGKPNVNSTKREKQKNGTLTVSTLPVGT 429
:
:
:
DB 121 LFIKSPITICLVVDLAPSKGTVNLTWRSRSGKPNVNSTKREKQKNGTLTVSTLPVGT 180
:
:
:
OY 430 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAAPVYAFATPEWPGSRDKRTLACLIQ 489
:
:
:
DB 181 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAAPVYAFATPEWPGSRDKRTLACLIQ 240
:
:
:
OY 490 NFMEDISVOMLHNEVOLDPARHSTTOPRRTKSGGFFVFSRLLEVTRAEMQKDEFICRAV 549
:
:
:
DB 241 NFMEDISVOMLHNEVOLDPARHSTTOPRRTKSGGFFVFSRLLEVTRAEMQKDEFICRAV 300
:
:
:
OY 550 HEAASPSQTVORAVSNPGK 569
:
:
:
DB 301 HEAASPSQTVORAVSNPGK 320
:
:
:
RESULT 11
US-09-949-375A-2
: Sequence 2, Application US/09949375A
: Patent No. US2002017267A1
: GENERAL INFORMATION:
: APPLICANT: KLYSNER, Steen et al.
: TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
: FILE REFERENCE: 3631-0111P
: CURRENT APPLICATION NUMBER: US/09/949,375A
: CURRENT FILING DATE: 2002-01-18
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
```

```
:
:
:
: LENGTH: 323
: TYPE: PRT
: ORGANISM: homo sapiens
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (8)..(103)
: OTHER INFORMATION: Human Ige heavy chain C2 domain
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (112)..(211)
: OTHER INFORMATION: Human Ige heavy chain C3 domain
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (216)..(317)
: OTHER INFORMATION: Human Ige heavy chain C4 domain
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (104)..(111)
: OTHER INFORMATION: Linker between domains C2 and C3
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (212)..(215)
: OTHER INFORMATION: Linker between domains C3 and C4
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (100)..(114)
: OTHER INFORMATION: Epitope including C2C3 linker
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (210)..(218)
: OTHER INFORMATION: Epitope including C3C4 linker
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (139)..(145)
: OTHER INFORMATION: Epitope in BC loop
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (167)..(175)
: OTHER INFORMATION: Epitope in DE loop
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (196)..(206)
: OTHER INFORMATION: Epitope in FG loop
: US-09-949-375A-2

Query Match 55.8%; Score 1707; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.9e-98;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 250 FTPTVKILQSSCGGHHFPTIOLCLVSGYTPGTINITWLEGGVMDVLDLSTASTOE 309
:
:
:
DB 4 FTPTVKILQSSCGGHHFPTIOLCLVSGYTPGTINITWLEGGVMDVLDLSTASTOE 63
:
:
:
OY 310 GELASTOSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCADSNPBGVSAIYLSRPSFD 369
:
:
:
DB 64 GELASTOSELTLSQKHWLSDRTYTCQVYOGHTEFEDSTKCADSNPBGVSAIYLSRPSFD 123
:
:
:
OY 370 LFIKSPITICLVVDLAPSKGTVNLTWRSRSGKPNVNSTKREKQKNGTLTVSTLPVGT 429
:
:
:
DB 124 LFIKSPITICLVVDLAPSKGTVNLTWRSRSGKPNVNSTKREKQKNGTLTVSTLPVGT 183
:
:
:
OY 430 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAAPVYAFATPEWPGSRDKRTLACLIQ 489
:
:
:
DB 184 RDWIEGETYOCRVTHPHLPALMRSTTKSGPRAAPVYAFATPEWPGSRDKRTLACLIQ 243
:
:
:
OY 490 NFMEDISVOMLHNEVOLDPARHSTTOPRRTKSGGFFVFSRLLEVTRAEMQKDEFICRAV 549
:
:
:
DB 244 NFMEDISVOMLHNEVOLDPARHSTTOPRRTKSGGFFVFSRLLEVTRAEMQKDEFICRAV 303
:
:
:
OY 550 HEAASPSQTVORAVSNPGK 569
:
:
:
DB 304 HEAASPSQTVORAVSNPGK 323
:
:
:
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| | | | | |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match | 55.8% | Score 1707; | DB 9; | Length 323; |
| Best Local Similarity | 100.0% | Pred. No. 8.9e-98; | | |
| Matches 320; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0 |

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RESULT 13
US-09-949-375A-6
; Sequence 6, Application US/09949375A
; Patent No. US20020172673a1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING ICE
; FILE REFERENCE: 3631-0111P
; CURRENT APPLICATION NUMBER: US/09/949,375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 5
US-09-949-375A-6

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| | | | | |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match | 55.8%; | Score 1707; | DB 9; | Length 323; |
| Best Local Similarity | 100.0%; | Pred. No. 8.9e-98; | | |
| Matches 320; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

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RESULT 14
US-10-176-664-1
; Sequence 1, Application US/10176664
; Publication No. US20030031663A1
;
GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/03/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
;
LENGTH: 331
;
TYPE: PRT
;
ORGANISM: Artificial Sequence
;
FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-1

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| | Query Match | 55.8% | Score 1707 | DB 9 | Length 331 |
|----|-----------------------|--|-------------------|----------|------------|
| | Best Local Similarity | 100.0% | Pred. No. 9,1e-98 | | |
| | Matches 320 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY | 250 | FPPPTVKILIOSCDGGGHPPTIQLLCLVSGYPTGTTINITWLEDQVMDVDLSTASTQE | 305 | | |
| DB | 12 | FTPTPTVKILIOSCGGGHPPTIQLLCLVSGYPTGTTINITWLEDQVMDVDLSTASTQE | 71 | | |
| QY | 310 | GELASTOSELTLSOKHMLSDRTYTCQVYTGQGHFFEDSTKCADSNPRGSAVLSNPSFD | 366 | | |
| DB | 72 | GELASTOSELTLSOKHMLSDRTYTCQVYTGQGHFFEDSTKCADSNPRGSAVLSNPSFD | 133 | | |
| QY | 370 | LFIRKSPITICLVVDLAPSKGVNLTWMSRASKPVNHSRKEKORNGTLVTVSTLPVGT | 422 | | |
| DB | 132 | LFIRKSPITICLVVDLAPSKGVNLTWMSRASKPVNHSRKEKORNGTLVTVSTLPVGT | 19 | | |
| QY | 430 | RDWIEGEYTCQRYTHPLPRALMRSTTKSGPAAAEYVAFTPMWPSRDKRTLACLIQ | 489 | | |
| DB | 192 | RDWIEGEYTCQRYTHPLPRALMRSTTKSGPAAAEYVAFTPMWPSRDKRTLACLIQ | 25 | | |
| QY | 490 | NFMEDISVOMLNEVOLDPARHSTTQPRKTKSGFVFSRLFVTRAEWOKDEFICRAV | 549 | | |
| DB | 252 | NFMEDISVOMLNEVOLDPARHSTTQPRKTKSGFVFSRLFVTRAEWOKDEFICRAV | 31 | | |

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 06:55:24 ; Search time 22.8412 Seconds
(without alignments)
732.958 Million cell updates/sec

Title: US-09-847-208B-7
Perfect score: 3060
Sequence: 1 EPKSCDKHTHPCPCAPPELL.....HEAAPSQTVQRAVSNPGK 569

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------------------------------|
| 1 | 1273.5 | 41.6 | 711 | 4 | US-09-485-737B-90 Sequence 90, Appl |
| 2 | 1232 | 40.3 | 660 | 4 | US-09-181-706-8 Sequence 8, Appl |
| 3 | 1232 | 40.3 | 660 | 4 | US-09-458-791-8 Sequence 8, Appl |
| 4 | 1232 | 40.3 | 660 | 4 | US-09-459-066-8 Sequence 8, Appl |
| 5 | 1225 | 40.0 | 232 | 2 | US-08-595-043A-50 Sequence 50, Appl |
| 6 | 1225 | 40.0 | 331 | 4 | US-09-178-869-2 Sequence 2, Appl |
| 7 | 1225 | 40.0 | 360 | 4 | US-09-180-100-11 Sequence 11, Appl |
| 8 | 1225 | 40.0 | 371 | 1 | US-08-236-311-7 Sequence 7, Appl |
| 9 | 1225 | 40.0 | 371 | 3 | US-08-457-918-7 Sequence 7, Appl |
| 10 | 1225 | 40.0 | 376 | 4 | US-09-180-100-22 Sequence 22, Appl |
| 11 | 1225 | 40.0 | 396 | 2 | US-08-784-512-3 Sequence 3, Appl |
| 12 | 1225 | 40.0 | 396 | 4 | US-09-176-228-3 Sequence 3, Appl |
| 13 | 1225 | 40.0 | 424 | 5 | PCT-US95-03866-12 Sequence 12, Appl |
| 14 | 1225 | 40.0 | 424 | 5 | PCT-US95-03866-14 Sequence 14, Appl |
| 15 | 1225 | 40.0 | 437 | 5 | PCT-US96-10043-11 Sequence 11, Appl |
| 16 | 1225 | 40.0 | 442 | 5 | PCT-US96-10043-9 Sequence 9, Appl |
| 17 | 1225 | 40.0 | 446 | 3 | US-08-397-411-7 Sequence 7, Appl |
| 18 | 1225 | 40.0 | 449 | 1 | US-08-458-516-13 Sequence 13, Appl |
| 19 | 1225 | 40.0 | 459 | 1 | US-08-157-101A-7 Sequence 7, Appl |
| 20 | 1225 | 40.0 | 476 | 2 | US-08-378-939-10 Sequence 10, Appl |
| 21 | 1225 | 40.0 | 476 | 3 | US-08-487-550-4 Sequence 4, Appl |
| 22 | 1225 | 40.0 | 476 | 3 | US-08-487-550-12 Sequence 12, Appl |
| 23 | 1225 | 40.0 | 478 | 3 | US-08-487-550-8 Sequence 8, Appl |
| 24 | 1220 | 39.9 | 254 | 2 | US-08-284-391B-33 Sequence 33, Appl |
| 25 | 1220 | 39.9 | 254 | 4 | US-09-218-950-33 Sequence 33, Appl |
| 26 | 1220 | 39.9 | 389 | 4 | US-09-131-247-14 Sequence 14, Appl |
| 27 | 1219 | 39.8 | 330 | 4 | US-09-301-593-22 Sequence 22, Appl |

| | | | | | |
|----|------|------|-----|---|-------------------------------------|
| 28 | 1219 | 39.8 | 451 | 2 | US-08-887-352B-14 Sequence 14, Appl |
| 29 | 1219 | 39.8 | 451 | 2 | US-08-887-352B-16 Sequence 16, Appl |
| 30 | 1219 | 39.8 | 451 | 2 | US-08-887-352B-18 Sequence 18, Appl |
| 31 | 1219 | 39.8 | 451 | 3 | US-08-466-151-65 Sequence 65, Appl |
| 32 | 1219 | 39.8 | 451 | 3 | US-09-109-207C-14 Sequence 14, Appl |
| 33 | 1219 | 39.8 | 451 | 4 | US-09-109-207C-16 Sequence 16, Appl |
| 34 | 1219 | 39.8 | 451 | 4 | US-09-109-207C-18 Sequence 18, Appl |
| 35 | 1219 | 39.8 | 451 | 4 | US-09-109-207C-16 Sequence 16, Appl |
| 36 | 1219 | 39.8 | 451 | 4 | US-09-054-255-2 Sequence 2, Appl |
| 37 | 1219 | 39.8 | 451 | 4 | US-09-296-005-14 Sequence 14, Appl |
| 38 | 1219 | 39.8 | 451 | 4 | US-09-296-005-16 Sequence 16, Appl |
| 39 | 1219 | 39.8 | 451 | 4 | US-09-296-005-18 Sequence 18, Appl |
| 40 | 1219 | 39.8 | 452 | 3 | US-09-027-449-71 Sequence 71, Appl |
| 41 | 1219 | 39.8 | 452 | 4 | US-09-026-985-71 Sequence 71, Appl |
| 42 | 1219 | 39.8 | 452 | 4 | US-09-121-952A-71 Sequence 71, Appl |
| 43 | 1219 | 39.8 | 452 | 4 | US-09-234-340A-71 Sequence 71, Appl |
| 44 | 1219 | 39.8 | 453 | 3 | US-08-466-151-8 Sequence 8, Appl |
| 45 | 1219 | 39.8 | 453 | 4 | US-08-466-153B-8 Sequence 8, Appl |

ALIGNMENTS

```
RESULT 1
US-09-485-737B-90
: Sequence 90, Application US/09485737B
: Patent No. 6350860
:
: GENERAL INFORMATION:
: APPLICANT: Bayse, Marie-Ange
: TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
: TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
: FILE REFERENCE: INNS:015
: CURRENT APPLICATION NUMBER: US/09/485,737B
: CURRENT FILING DATE: 2000-02-14
: PRIOR APPLICATION NUMBER: PCT/EP 98/05165
: PRIOR FILING DATE: 1998-08-14
: PRIOR APPLICATION NUMBER: EPO 98870139.7
: PRIOR FILING DATE: 1998-06-18
: PRIOR APPLICATION NUMBER: EPO 97870122.5
: PRIOR FILING DATE: 1997-08-18
: NUMBER OF SEQ ID NOS: 104
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 90
: LENGTH: 711
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90
Query Match 41.6%; Score 1273.5; DB 4; Length 711;
Best Local Similarity 50.1%; Pred. No. 2.5e+99;
Matches 286; Conservative 45; Mismatches 109; Indels 131; Gaps 16;
1 EPKSCDKHTHPCPCAPPELLGSPVFLPPPKDTLMSRPEVVCVVVDVSHEDPEYK 60
236 EPKSCDKHTHPCPCAPPELLGSPVFLPPPKDTLMSRPEVVCVVVDVSHEDPEYK 295
61 NMYVDGVEHNVKTPREDOYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAIEKT 120
236 NMYVDGVEHNVKTPREDOYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAIEKT 355
121 ISKAVDQREPOVYTLPPSRDELTKNOVSLTCTLVGFGYPSDIAVWESNGOENNPKTP 180
356 ISKAVDQREPOVYTLPPSRDELTKNOVSLTCTLVGFGYPSDIAVWESNGOENNPKTP 415
181 PYLDVGSEFFLYSKLTVDKSRWQGNVSCSYMHALHNHYQORSLSPGKVEGGGSG 240
416 PYLDVGSEFFLYSKLTVDKSRWQGNVSCSYMHALHNHYQORSLSPGKVEGGGSG 468
241 GGGSGGGSGFPPTVYKIIQSSCD---GGGHPPTIQLCLVSGYPTPTINTWLED--- 293
```

Db 469 -----GGGS-----QVQLVQSGSELKPKGA-----SVKISCKASGTYFTDYGMNWKQAPG 514
QY 294 -----GQMDVD-----ISTASTQGEELASTQSELTLISQKHWLSDRT 331
Db 515 QGLKMGMINVTYESTESTYDFKGFYFSLDTVSAAALQISSILKAEDT-----AT 565
QY 332 YTC-----QVLYGHFPEDSTKCADSNPRGVSATYLSRPPDLFIKSPITITCLVVDL 385
Db 566 YFCARRGYANDYMG-----QGTIVTVSSGGSGGGGGGGSDIVLTQSPA----- 613
QY 386 APSKGYVLTWSRASGKPVNSTRKEKQKNGTLTVSTLTPVGTTRDWIEGETYOCRVTHP 445
Db 614 -----TMSASPGERV-----TLTCSASSISYWFVYHQRPGS----- 646
QY 446 HLPALMRSTK-TSGPRAPEVYAFATPEWPGSRDKRTTLACLIONFEDISVQWMLNE 504
Db 647 --PLLIVTISNLSAGVA-----RPSGSGSGTSYSLTISRMEPEDFAYFYCHOS 694
QY 505 VQLPDARHSTQPRKTKSGGFVFSRLLEVTR 535
Db 695 SSYP-----FTFGQG-----TKLEIKR 711

RESULT 2
US-09-181-706-8
; Sequence 8, Application US/09181706
; Patent No. 6130068
; GENERAL INFORMATION:
; APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
; APPLICANT: Robert F. Dubose, Richard S. Johnson
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC-compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/181,706
; FILING DATE: October 28, 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/958,598 (converted to a
; APPLICATION NUMBER: Provisional, see below)
; FILING DATE: October 28, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
; APPLICATION NUMBER: conversion to provisional application)
; FILING DATE: October 26, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-181-706-8

Query Match 40.3%; Score 1232; DB 4; Length 660;
Best Local Similarity 93.0%; Pred. No. 7.2e-96;
Matches 227; Conservative 7; Mismatches 8; Indels 2; Gaps 1;
QY 1 EPKSGDKHPCPCPAPPELLGSPSYFLEPPPKKOTLMSTRPEYTCVYVDVSHDEPEYK 60
Db 32 DKRSCDKHTPCPCPAPBAGPVSFLEPPPKKOTLMSTRPEYTCVYVDVSHDEPEYK 91
QY 61 NMVYDGEVHAKTKPREQYNSTRVYVSVTLVHONMNGKREYCKSNKALPAPIEKT 120
Db 92 NMVYDGEVHAKTKPREQYNSTRVYVSVTLVHODMLNGKREYCKSNKALPAPIEKT 151
QY 121 ISKAKVQPREQVYTLTPSRDELTKNOVSLTCLVKGFTYPSDIAVWESNGOPENNYKTP 180
Db 152 ISKAKQPREQVYTLTPSRREMKNOVSLTCLVKGFTYPSDIAVWESNGOPENNYKTP 211
QY 181 PVLDSVGSFFLYSKLTVDRKMOQGNVSCSVMEHALHNHYOQSLSPKVGSGSG 240
Db 212 PVLDSGGSFFLYSKLTVDRKMOQGNVSCSVMEHALHNHYOQSLSPKVGSGSG 269
QY 241 GGGS 244
Db 270 GGGS 273

RESULT 3
US-09-458-791-8
; Sequence 8, Application US/09458791
; Patent No. 6174689
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/458,791
; FILING DATE: 10-Dec-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE: 28-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-458-791-8

Query Match 40.3%; Score 1232; DB 4; Length 660;
Best Local Similarity 93.0%; Pred. No. 7.2e-96;
Matches 227; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

Db 181 PVLDSGSEFLYSLKTYDKSRMOGNNFSCVMHEALHNHYTKSLSPGK 232

RESULT 6
US-09-178-869-2
Sequence 2, Application US/091788698
Patent No. 6197294
GENERAL INFORMATION:
APPLICANT: Tao, Meng
APPLICANT: Wong, Shou
APPLICANT: Hickey, Joseph P.
APPLICANT: Baetge, E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043
CURRENT APPLICATION NUMBER: US/09/178, 869B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 331
TYPE: PRT
ORGANISM: Homo sapiens
US-09-178-869-2

Query Match 40.0%; Score 1225; DB 4; Length 331;
Best Local Similarity 97.0%; Pred. No. 1e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDTHHCPCPAPPELLGSPVFLPPKPKDTLMISRPEVTCVAVDVSHDDPEVKF 60
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Db 100 EPKSCDTHHCPCPAPPELLGSPVFLPPKPKDTLMISRPEVTCVAVDVSHDDPEVKF 159
|||||
Qy 61 NMVYDGEVHNVTKPREEQYNSTYRVSVLTVLHOMMNGKEKCKYSNKALPAPIEKT 120
|||||
Db 160 NMVYDGEVHNVTKPREEQYNSTYRVSVLTVLHOMMNGKEKCKYSNKALPAPIEKT 219
|||||
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGOPENNYKTP 180
|||||
Db 220 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGOPENNYKTP 279
|||||
Qy 181 PVLDSGSEFLYSLKTYDKSRMOGNNFSCVMHEALHNHYTKSLSPGK 232
|||||
Db 280 PVLDSGSEFLYSLKTYDKSRMOGNNFSCVMHEALHNHYTKSLSPGK 331
|||||

RESULT 7
US-09-180-100-11
Sequence 11, Application US/09180100
Patent No. 6306395
GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 630639510
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180, 100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-180-100-11

Query Match 40.0%; Score 1225; DB 4; Length 360;
Best Local Similarity 97.0%; Pred. No. 1.2e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDTHHCPCPAPPELLGSPVFLPPKPKDTLMISRPEVTCVAVDVSHDDPEVKF 60

Db 129 EPKSCDTHHCPCPAPPELLGSPVFLPPKPKDTLMISRPEVTCVAVDVSHDDPEVKF 188
|||||

Qy 61 NMVYDGEVHNVTKPREEQYNSTYRVSVLTVLHOMMNGKEKCKYSNKALPAPIEKT 120
|||||

Db 189 NMVYDGEVHNVTKPREEQYNSTYRVSVLTVLHOMMNGKEKCKYSNKALPAPIEKT 248
|||||

Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGOPENNYKTP 180
|||||

Db 249 ISKAKGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGOPENNYKTP 308
|||||

Qy 181 PVLDSGSEFLYSLKTYDKSRMOGNNFSCVMHEALHNHYTKSLSPGK 232
|||||

Db 309 PVLDSGSEFLYSLKTYDKSRMOGNNFSCVMHEALHNHYTKSLSPGK 360
|||||

RESULT 8
US-08-236-311-7
Sequence 7, Application US/08236311
Patent No. 5565335
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adhesion Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236, 311
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28, 616
REFERENCE/DOCKET NUMBER: 444PIC2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-236-311-7

Query Match 40.0%; Score 1225; DB 1; Length 371;
Best Local Similarity 97.0%; Pred. No. 1.2e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDTHHCPCPAPPELLGSPVFLPPKPKDTLMISRPEVTCVAVDVSHDDPEVKF 60

Db 140 EPKSCDKHTHCPPCAPAPELLGSPVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 199
QY 61 NMVYDGEVHNKTKPREQYNSTYRVYSVLTVLIHQNMNGKEKCKYSNNALPAPIEKT 120
Db 200 NMVYDGEVHNKTKPREQYNSTYRVYSVLTVLIHQDLNGEKYCKYSNNALPAPIEKT 259
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFFPSDIAVEMESNGOPENNYKTP 180
Db 260 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFFPSDIAVEMESNGOPENNYKTP 319
QY 181 PVLDSVGSFFLYSKLTVDKSRMOQGNVSCSVMEHALHNHYOQSLSPGK 232
Db 320 PVLDSGSEFFLYSKLTVDKSRMOQGNVSCSVMEHALHNHYOQSLSPGK 371

RESULT 9
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubienc, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444PIC3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-457-918-7

Query Match 40.0%; Score 1225; DB 3; length 371;
Best Local Similarity 97.0%; Pred. No. 1.2e-95;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKHTHCPPCAPAPELLGSPVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 60
Db 140 EPKSCDKHTHCPPCAPAPELLGSPVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 199
QY 61 NMVYDGEVHNKTKPREQYNSTYRVYSVLTVLIHQNMNGKEKCKYSNNALPAPIEKT 120
Db 200 NMVYDGEVHNKTKPREQYNSTYRVYSVLTVLIHQDLNGEKYCKYSNNALPAPIEKT 259
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFFPSDIAVEMESNGOPENNYKTP 180
Db 260 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFFPSDIAVEMESNGOPENNYKTP 319
QY 181 PVLDSVGSFFLYSKLTVDKSRMOQGNVSCSVMEHALHNHYOQSLSPGK 232
Db 320 PVLDSGSEFFLYSKLTVDKSRMOQGNVSCSVMEHALHNHYOQSLSPGK 371

RESULT 10
US-09-180-100-22
; Sequence 22, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-22

Query Match 40.0%; Score 1225; DB 4; length 376;
Best Local Similarity 97.0%; Pred. No. 1.2e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKHTHCPPCAPAPELLGSPVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 60
Db 145 EPKSCDKHTHCPPCAPAPELLGSPVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKF 204
QY 61 NMVYDGEVHNKTKPREQYNSTYRVYSVLTVLIHQNMNGKEKCKYSNNALPAPIEKT 120
Db 205 NMVYDGEVHNKTKPREQYNSTYRVYSVLTVLIHQDLNGEKYCKYSNNALPAPIEKT 264
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFFPSDIAVEMESNGOPENNYKTP 180
Db 265 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFFPSDIAVEMESNGOPENNYKTP 324
QY 181 PVLDSVGSFFLYSKLTVDKSRMOQGNVSCSVMEHALHNHYOQSLSPGK 232
Db 325 PVLDSGSEFFLYSKLTVDKSRMOQGNVSCSVMEHALHNHYOQSLSPGK 376

RESULT 11
US-08-784-512-3
; Sequence 3, Application US/08784512
; Patent No. 5872209
; GENERAL INFORMATION:
; APPLICANT: BARTNIK, Eckart
; APPLICANT: EIDENMUELLER, Bernd
; APPLICANT: BUETTNER, Frank
; APPLICANT: CATERSON, Bruce
; APPLICANT: HUGHES, Clare
; TITLE OF INVENTION: An artificial recombinant substrate (rAGC 1)
; TITLE OF INVENTION: and native aggregate to study the proteolytic activity of

```

; TITLE OF INVENTION: "Aggrecanase" in cell culture systems
;
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,512
; FILING DATE: 17-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 96100682.2
; FILING DATE: 18-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..396
; US-08-784-512-3
;
; Query Match 40.0%; Score 1225; DB 2; Length 396;
; Best Local Similarity 97.0%; Pred. No. 1.3e-95;
; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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; QY 1 EPKSCDTHTCPCPAPPELLGSPVFLPPPKDITLMSRTPEVTCVAVDVSHDDPEYKF 60
; DB 165 EPKSCDTHTCPCPAPPELLGSPVFLPPPKDITLMSRTPEVTCVAVDVSHDDPEYKF 224
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; QY 61 NMVYDGEVHNHAKTKPREQYNSTYRVVSVLTVLIHOMMNGKEKCKVSNKALPAPIEKT 120
; DB 225 NMVYDGEVHNHAKTKPREQYNSTYRVVSVLTVLIHOMMNGKEKCKVSNKALPAPIEKT 284
;
; QY 121 ISKAKVQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTP 180
; DB 285 ISKAKGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTP 344
;
; QY 181 PVLDSVGSFELYSKLITVDKSRMOQGNVFCSCVMHEALHNHYYQKSLSPCK 232
; DB 345 PVLDSGSEFLYSKLITVDKSRMOQGNVFCSCVMHEALHNHYYQKSLSPCK 396
;
; RESULT 12
; US-09-176-228-3
; Sequence 3, Application US/09176228
; Patent No. 618034
; GENERAL INFORMATION:
; APPLICANT: BARTNIK, Eckart
; APPLICANT: EIDENMUELLER, Bernd
; APPLICANT: BUETTNER, Frank
; APPLICANT: CATERSON, Bruce
; APPLICANT: HUGHES, Clare
; TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
; TITLE OF INVENTION: and native aggrecan to study the proteolytic activity of
; TITLE OF INVENTION: "Aggrecanase" in cell culture systems

```

```

; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/176,228
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,512
; FILING DATE: 17-JAN-1997
; APPLICATION NUMBER: EP 96100682.2
; FILING DATE: 18-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..396
; US-09-176-228-3
;
; Query Match 40.0%; Score 1225; DB 4; Length 396;
; Best Local Similarity 97.0%; Pred. No. 1.3e-95;
; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
;
; QY 1 EPKSCDTHTCPCPAPPELLGSPVFLPPPKDITLMSRTPEVTCVAVDVSHDDPEYKF 60
; DB 165 EPKSCDTHTCPCPAPPELLGSPVFLPPPKDITLMSRTPEVTCVAVDVSHDDPEYKF 224
;
; QY 61 NMVYDGEVHNHAKTKPREQYNSTYRVVSVLTVLIHOMMNGKEKCKVSNKALPAPIEKT 120
; DB 225 NMVYDGEVHNHAKTKPREQYNSTYRVVSVLTVLIHOMMNGKEKCKVSNKALPAPIEKT 284
;
; QY 121 ISKAKVQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTP 180
; DB 285 ISKAKGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTP 344
;
; QY 181 PVLDSVGSFELYSKLITVDKSRMOQGNVFCSCVMHEALHNHYYQKSLSPCK 232
; DB 345 PVLDSGSEFLYSKLITVDKSRMOQGNVFCSCVMHEALHNHYYQKSLSPCK 396
;
; RESULT 13
; PCT-0595-03866-12
; Sequence 12, Application PC/TUS9503866
; GENERAL INFORMATION:
; APPLICANT: CytoMed, Inc. (all states except US)
; APPLICANT: CytoMed, Inc. (US only)
; APPLICANT: Nocke, Karl (US only)
; APPLICANT: Lobell, Robert B (US only)
; TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
; TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave

```

STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cytomed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-03866-12

Query Match 40.0%; Score 1225; DB 5; Length 424;
Best Local Similarity 97.0%; Pred. No. 1.5e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMSRPEVTGVVVDVSHEDPEVKF 60
DB 193 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMSRPEVTGVVVDVSHEDPEVKF 252

QY 61 NMVYDGVGVHNKTKPREBOYNSTRVYSVLTVLHONMMNGKEYCKSNKALPAPIEKT 120
DB 253 NMVYDGVGVHNKTKPREBOYNSTRVYSVLTVLHODWLNGKEYCKSNKALPAPIEKT 312

QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEMESNGOPENNYKTTT 180
DB 313 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEMESNGOPENNYKTTT 372

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSVMHBALNHNHYQORSLSPGK 232
DB 373 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSVMHBALNHNHYQORSLSPGK 424

RESULT 14
PCT-US95-03866-14
Sequence 14, Application PC/TUS9503866
GENERAL INFORMATION:
APPLICANT: Cytomed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cytomed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-03866-14

Query Match 40.0%; Score 1225; DB 5; Length 424;
Best Local Similarity 97.0%; Pred. No. 1.5e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMSRPEVTGVVVDVSHEDPEVKF 60
DB 193 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMSRPEVTGVVVDVSHEDPEVKF 252

QY 61 NMVYDGVGVHNKTKPREBOYNSTRVYSVLTVLHONMMNGKEYCKSNKALPAPIEKT 120
DB 253 NMVYDGVGVHNKTKPREBOYNSTRVYSVLTVLHODWLNGKEYCKSNKALPAPIEKT 312

QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEMESNGOPENNYKTTT 180
DB 313 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEMESNGOPENNYKTTT 372

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSVMHBALNHNHYQORSLSPGK 232
DB 373 PVLDSVGSFFLYSKLTVDKSRWQGNVSCSVMHBALNHNHYQORSLSPGK 424

RESULT 15
PCT-US96-10043-11
Sequence 11, Application PC/TUS9610043
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,213
FILING DATE: 14-JUN-1995
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 00786/284001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10043-11

Query Match 40.0%; Score 1225; DB 5; Length 437;
Best Local Similarity 97.0%; Pred. No. 1.5e-95;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | EPKSCDKTHTCPPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF | 60 |
| DB | 206 | EPKSCDKTHTCPPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF | 265 |
| QY | 61 | NWYVDGVEVHNAKTKRPREQYNSTYRVVSVLTVLHQDTMISRTPEVTCVVVDVSHEDPEVKF | 120 |
| DB | 266 | NWYVDGVEVHNAKTKRPREQYNSTYRVVSVLTVLHQDTMISRTPEVTCVVVDVSHEDPEVKF | 325 |
| QY | 121 | ISKAKVQPREPVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEMESNGOPENNYKTTT | 180 |
| DB | 326 | ISKAKVQPREPVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEMESNGOPENNYKTTT | 385 |
| QY | 181 | PVLDSVGSFELYSKLTVDKSRMQGNVFSQVMHEALHNHYQOORSLSPGK | 232 |
| DB | 386 | PVLDSVGSFELYSKLTVDKSRMQGNVFSQVMHEALHNHYQOORSLSPGK | 437 |

Search completed: July 15, 2003, 07:02:42
Job time : 23.8412 secs